Factors Influencing the Survival of Pathogenic Microbes in the Built (i.e. hospitals) and Natural Environments

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In the name of Allah, the Most Merciful, the Most Kind

Dedication

I dedicated this work to my parents (Nahlah Khawajh, Abdulrahim Alaeq) who continue to learn, grow and develop and who has been a source of encouragement and inspiration to me throughout my life. Also, I am grateful to my sisters: Roaa, Rola, Rawan, and Reman and my brothers Ali and Rakan and my friends for their spiritual support and encouragement.

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ABSTRACT

Healthcare associated infections, i.e. nosocomial infections, occur in patients under medical care. These infections occur during stays in hospital and cause prolonged hospitalisation, disability, and an economic burden. Nosocomial pathogens include bacteria, viruses and fungal parasites. Pathogens living in the healthcare environment and equipment can be an obvious source of pathogen transmission. These pathogens can be transmitted by person to person contact or via contaminated water and food, infected individuals, contaminated healthcare personnel's skin or contact via shared items and surfaces. Pathogens can survive in the hospital environment for long periods and, in some cases, resist disinfection. Bacteria are the most common pathogens responsible for nosocomial infections. The Thesis begins with a description of the aims of the work, followed by studies the distribution of bacteria in the environment and their survival in the healthcare settings, the determination of the number of bacteria on hands after washing and drying normally and following the use of a warm air dryer. The factors which influence the survival of bacteria and *Candida* in the built environment were also determined on ceramic tiles, copper and plastic plumbing surfaces, and on new toothbrushes. Pathogenic bacteria were isolated from used toothbrushes and the effect of toothpastes on the growth of pathogenic bacteria was determined, as was the effectiveness of antibacterial cloths in inhibiting the growth of bacteria and yeast. The metabolic diversity of the bacterial isolates was also determined. Bacteria were isolated from a range of surfaces commonly found in hospitals and health care settings. A wide variety of bacteria were isolated from sinks, computer keyboards and computer mice, taps and the surface of mobile phones and toilet mirrors. Species of *Bacillus* were exclusively isolated from vacuum cleaner dust and from books and dust obtained from a library. Bacteria other than just *Bacillus* were isolated from the soles of shoes. Lift buttons were found to be contaminated with bacteria, not surprisingly

with species which are typically skin commensals, with the number being highest on the ground floor-call button. Bacteria were found to be spread by hot-air hand dryers, both into the toilet environment and onto previously washed hands. It is provisionally recommended that disposable paper towels are used in preference to such machines. Bacteria and the yeast, *Candida rugosa* survived when inoculated onto both rough and smooth tile surfaces similar to those used in health care settings. A wide range of potentially pathogenic bacteria were isolated from used toothbrushes and the survival of inoculated bacteria on tooth brushes was determined. The bacteria were shown to survive for varying periods, a finding of some concern in relation to dental hygiene. A range of toothpastes were also shown to be antibacterial. The survival of inoculated bacteria on copper and plastic surfaces typically used as piping in health care settings was determined. Copper surfaces were shown to be antibacterial, while plastic surfaces were not. It is therefore suggested that in critical healthcare areas, copper piping should be given preference over the plastic variety. Proprietary antibacterial clothes were tested for their antibacterial properties. Despite being marketed for this purpose, the cloths showed no obvious, marked antibacterial activity.

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CHAPTER 1

DISTRIBUTION AND SURVIVAL OF BACTERIA IN HEALTHCARE SETTINGS

1.1 Introduction

A wide range of microorganisms can be isolated from the environment, including bacteria, viruses, filamentous fungi and yeasts. Particular emphasis has been placed on the role of bacteria in medicine, but fungi (including yeasts) are also causal agents of many plant and animal diseases although their role as human pathogens is often underplayed. In a recent study setting (Perlroth *et al*., 2007), for example, fungi were estimated to kill at least as many people as tuberculosis or malaria, over the past decades. The pathogenicity of both bacteria and yeasts is particular potentially dangerous in the case of immunocompromised patients, in which they cause potentially life-threatening diseases (Sullivan *et al.*, 1997).

A **hospital-acquired infections** (**HAIs**), also known as a **nosocomial infection**, are acquired in health care facilities. Health care staff can spread infection, as can contaminated equipment, bed linens, or air droplets (McBryde *et al*., 2004). The infection can originate from the outside environment, infected patients or staff or in some cases the source of the infection is unknown. The microorganism may originate from the patient's own skin microflora, becoming opportunistic after surgery or other procedures that compromise the protective barrier of the skin. It is estimated that in The US around 1.7 million hospital-associated infections occur

and contribute to 99,000 deaths each year. Nosocomial infections can cause severe pneumonia and infections of the bloodstream, urinary tract and other areas of the body. Many of these infections are difficult to treat with antibiotics (Klevens *et al.*, 2007).

1.2 Organisms involved

Methicillin resistant *Staphylococcus aureus, Candida albicans, Pseudomonas aeruginosa, Acinetobacter baumannii, Stenotrophomonas maltophilia, Clostridium difficile, Escherichia coli,* and Vancomycin-resistant *Enterococcus.*

1.3 Sterilization

Sterilization kills all microbes on equipment and surfaces through exposure to chemicals, ionizing radiation, dry heat, or steam under pressure.

1.4 Isolation

Isolation precautions are designed to prevent transmission of microorganisms by common routes in hospitals. It involves the isolation of infectious cases in special hospitals and patients with infected wounds and joint transplantation patients in specific rooms. The following are important considerations regarding hygiene in health-care settings:

1.4.1 Handwashing

Handwashing is frequently the single most important act which reduces the risks of transmitting skin microorganisms between people or from one site to another on the same patient (Hugonnet *et al*., 2002). Prompt, thorough washing of hands between patient contacts and after contact with blood, body fluids, secretions, excretions, and equipment or articles contaminated by them is a major component of infection control and isolation (Katz, 2004). The spread of nosocomial infections, among immunocompromised patients is linked to health care workers' hand contamination in nearly half of all hands requires correct hand-hygiene procedures flora. The first relates to microbes picked up by workers from the environment which can survive on human skin and sometimes to grow (Katz, 2004). The second group is represented by the permanent microbes living on the skin surface which have low pathogenicity and infection rate, and can prevent colonization by more pathogenic bacteria; microbes making up the resident flora include: *Staphylococcus epidermidis*, *S. hominis*, and *Micrococcus*, *Propionibacterium*, *Corynebacterium*, *Dermobacterium*, and *Pitosporum spp*., while transient organisms comprise, *S. aureus*, and *Klebsiella pneumoniae*, and *Acinetobacter*, *Enterobacter* and *Candida* spp. Hand hygiene is aimed at eliminating the transient flora using a careful and dedicated hand washing with different kinds of soap, (normal and antiseptic), and alcohol-based gels. The lack of available sinks and time-consuming performance of hand washing presents problems related to its effectiveness (Langley, 2002).

1.4.2 Use of gloves

As well as hand washing, gloves play an major role in reducing the risks of microbial transmission. Gloves are worn to reduce the chance that microorganisms present on the hands of personnel can be transmitted to patients during invasive or other patient-care procedures and are also worn to limit the likelihood that the hands of personnel contaminated with microbes from a patient transmits the to another patient. Gloves must be changed between patient contacts, and hands should be washed after glove removal.

The wearing of gloves does not replace the need for handwashing, because gloves may have undetectable defects and hands can also become contaminated during glove removal; failure to change gloves between patient contacts is an obvious infection control hazard.

1.4.3 Antimicrobial surfaces

Microbes can survive on inanimate 'touch' surfaces for long periods, a fact which is troublesome in hospital environments in which patients with immunodeficiency are at increased risk of contracting nosocomial infections.

Common touch surfaces include bed rails, call buttons, touch plates, chairs, door handles, light switches, grab rails, intravenous poles, dispensers (alcohol gel, paper towel, soap), dressing trolleys, and counter and table tops are known to be contaminated with *Staphylococcus*, MRSA and vancomycin resistant *Enterococcus* (VRE) (Chemaly *et al.*, 2014). A number of compounds can

decrease the risk of bacteria growing on surfaces including: copper, silver, and germicides such as hydrogen peroxide vapour (Otter and French, 2009).

Nosocomial infections in the blood can cause serious medical problem and can result in major health care expenditure and death. The onset of infections in the bloodstream can be exacerbated by the previous use of antibiotics, corticosteroids, and a variety of chemotherapeutic agents. Major medical problems such cancers; neutropenia are also associated with increased problems from blood infections as is surgery and haemodialysis (Khan *et al.*, 2015).

The hospital environment is a potential reservoir of bacterial pathogens which are able to infect patients with a diverse variety of pathogenic microbes and thereby expose a large number of susceptible individuals to significant morbidity and mortality. Bacterial pathogens have an innate ability to survive for long periods on surfaces in the hospital environment (Dancer, 2009). Bacterial pathogens, isolated from hospital environment, are also beginning to develop resistance to multiple antimicrobial agents; these then cause difficulty in the treatment of nosocomial infections. The environment of patients is, as a result, heavily contaminated by infectious multidrug resistant organisms including methicillin-resistant *S. aureus* (MRSA), vancomycin-resistant Enterococci (VRE), *Clostridium difficile*, *Acinetobacter baumannii* and *Pseudomonas aeruginosa*, all of which are emerging to produce a major problem for healthcare systems (Dancer, 2009).

Infections in hospitals are, in the main, caused by factors such as cross-contamination between medical personnel, patients and visitors. Hospital surfaces

and equipment can also act as major reservoirs and sources of such cross infection (Cesar-Pastor *et al.*, 2012). Ubiquitous pathogens such as bacteria (*Escherichia coli, Enterococcus spp, Acinetobacter spp*, species of *Pseudomonas* and *Staphylococcus aureus*), viruses (e.g. noroviruses) and fungi (notably *Candida*) are particularly troublesome in the hospital environment because of the way they can survive for long periods on surfaces or humans (Thomas *et al.*, 2004). The uniforms of medical staff are often contaminated with multi-resistant *Staphylococcus aureus* and thereby provide a source of cross contamination (Boyce *et al.*, 1997). Air conditioning systems also act as source of airborne fungi such as species of *Aspergillus*, which can cause lung problems, especially amongst immunocompromised patients (Thomas *et al.*, 2004). Temperature is also a factor in the spread and development of hospital disease, especially in over-heated and under-ventilated environments which are often associated with the hospital environment, notably in winter (Ribera *et al.*, 1994).

1.5 Pathogen transmission

The transmission of contaminated pathogens on environmental surfaces is dependent on many factors including: the ability of pathogens to remain viable on dry surfaces; their ability to remain virulent after environmental exposure; the ability to colonize patients; the ability to transiently colonize the hands of health care workers and finally, the ability to develop resistance to disinfectants used on environmental surfaces (Weber *et al.*, 2010). Bacteria are transmitted by direct

contact between hands, body fluids such as saliva and mucus droplets; dust contaminated by bacteria in the air; via patient carers and via contaminated objects or equipment (Ortega *et al.,* 2010)

1.6 Survival of bacteria

Pathogens are able to survive in the hospital environment for long periods and, in some cases, resist disinfection. The frequency of environmental contamination with multi-resistant bacteria is greater for patients with infected wounds or were supplied with urinary drainage systems. Gastmeier *et al.* (2006) showed a correlation between survival time and diversity of important nosocomial pathogens. Most Gram-positive bacteria can survive for months on dry surfaces; *Enterococcus spp.* (including VRE) for example, can survive for 5 days to 4 months, *Staphylococcus aureus* remains viable for from 7 days to 7 months and *Streptococcus pyogens* survives for 3 days to 6.5 months. Many Gram-negative species can also survive for several months. *Acinetobacter spp*. for example, can survive for 3 days to 5 months on environmental surfaces, *Escherichia coli* persist for 16 months, while *Klebsiella spp.* remain viable for more than 30 months (Kramer *et al.*, 2006). Vancomycin-resistant *Enterococcus* (VRE) can remain viable on inanimate surfaces from seven days to two-four months (Burke, 2010). The duration of bacterial survival depends on the bacteria concerned and the nature of the contaminated surfaces. For example, Enterococci survive for more than 24h on bed-frames, 18h on cotton, 1h on telephones, 30 min on the diaphragm of a stethoscope, and 1 hour on gloves and hands (Talon, 1999).

Vancomycin-resistant *Enterococcus* have also been recovered from 3 of 10 seat cushions located in a room occupied by a VRE patient.

1.7 Responses of microorganisms to stress

Microbial cells sense stress in order to protect themselves against the deleterious effects of heat (56ºC), freeze–thaw injury, chemical or osmotic shock, exposure to reactive oxygen and nitrogen and to antimicrobial peptides or proteins. These responses involve physiological adaptations that counterbalance damage and allow the cells to continue to survive and grow (Griffiths, 2005). Entry into the stationary phase produces a general stress response, resulting in microbial resistance to multiple stresses. For example, when *Escherichia coli* is exposed to a sub-lethal stress, some of the cells die while some can be recovered on growth media. Growth of the recovered cell is dependent on a number of factors, including the level of stress, the nature of the recovery conditions and the growth phase of cell when the stress was imposed (Griffiths, 2005). Stationary phase cells show a greater tolerance to stress than exponentially growing ones. *E. coli* cells become shorter and rounder, the mode of metabolism alters and changes in membrane and cell wall structure occur (Griffiths, 2005). This response is seen in facultative anaerobes such as *Salmonella* and *Staphylococcus aureus* but generally not in strictly fermentative organisms such as *Streptococcus mutans*. *Campylobacter jejuni* also shows a reduced resistance during the stationary phase (Griffiths, 2005).

1.8 Responses of microorganisms to stress include:

1- Synthesis of protective proteins that repair cell damage, cell maintenance and bring about the eradication of stress agents.

2- Increases in resistance to lethal factors.

3- Transformation of cells to a latent state, e.g. the formation of spores.

4- Evasion of the host's defence mechanisms.

5- The production of adaptive mutations.

1.8.1 Types of microbial stress adaptation

The mechanisms of bacterial defence against environmental conditions are divided into two classes:

1- Limited or specific adaptive response resulting from microbial exposure to physical, chemical or biological stress, which protects cells against the subsequent lethal effects following the same stress (Griffiths, 2005).

2- Multiple adaptive responses (cross-protection) which occur when bacterial cells adapt to an inherent physiological condition or to an environmental factor, which results in microbial protection against subsequent lethal treatments, including stresses to which the microorganism had not been previously exposed. This type of protection is produced by a variety of stress conditions such as cell starvation,

exposure to high or low temperatures, high osmolality, and low pH (De Angelis and Gobbetti, 2004).

1.8.2 Starvation-stress response

When *E. coli*, *Salmonella*, and many other microorganisms are starved, they respond by inducing the expression of up to 50 new proteins or pre-existing proteins. The genetic and physiologic reprogramming that occurs is termed the starvation-stress response (SSR). The SSR allows for long term starvation survival of bacteria and provides generalized cross-resistance to a variety of other environmental stresses. In order to protect bacteria from damage, physiologic changes that occur during SSR include; the degradation of cellular RNA, proteins, and fatty acids; the reduction in the number of ribosomes; alterations in the amounts and type of nine lipids in the cytoplasmic membrane; an increase amounts of lipopolysaccharide in the outer membrane of Gram-negative bacteria; and increase the concentration of chromosomal DNA (Griffiths, 2005).

1.9 Epidemiologically significant pathogens

1.9.1 Bacteria

The main reservoirs for MRSA are infected patients and personnel in hospitals, and not surprisingly, the degree of pathogen contamination directly relates to the degree of localised infection in patients and on bandages, urine or blood. Both *Staphylococcus aureus* and MRSA can survive for up to nine weeks

(Popovich *et al.*, 2008). *Staphylococcus aureus* causes a variety of infections including skin, soft tissue infections, BSIs (blood stream infections), pneumonia, meningitis, endocarditis, and toxic shock syndrome (Popovich *et al.*, 2008). Coagulase-Negative Staphylococci (CoNS) are able to form biofilms on foreign devices located within patients, including prosthetic joints, pacemakers, intravenous catheters and shunts (Cervera *et al.*, 2009). Hidron *et al.* (2008) found that CoNS are easily the most frequent cause of central line-linked blood system infections (CLABSIs) and the second most common cause of surgical site infections (SSIs). Less commonly, CoNS infections result in catheter associated urinary tract infections (CA-UTIs) and ventilator-associated pneumonias (VAPs) (Martin *et al.*, 1989). These types of infections are now seen as increasingly common their occurrence has increased with the use of inter-body devices. Wisplinghoff *et al.* (2004) concluded that 9% of CLABSIs are caused by *Enterococcus* species, of which 2% of *E. faecalis* isolates; 60% of *E. faecium* isolates were found to be vancomycin resistant. VRE contamination has been found in up to 37% of samples obtained from the environment associated with gowns, health care workers, medical equipment, and microsphere beds. *Clostridium difficile* spores are durable and resistant to unusual cleaning methods and contamination of the hospital environments by spores has been reported. Such spores are highly resistant and may survive for months in the environment. Hospital floors remain contaminated with these spores for up to five months and contamination density is increased by presence of patients infected with diarrhea

(Hidron *et al.*, 2008). The gastrointestinal tract of young people is a reservoir of *C. difficile* which is transmitted via the faecal-oral route, directly by hand carriage by health care workers (HCWs), or by patient-to-patient contact or indirectly from a contaminated environmental source (Burke, 2010). Best *et al.* (2010) sampled the air and environmental surfaces adjacent to patients with symptomatic CDI and found *C. difficile* near a majority of the patients. Clinicians around the world have noted an increase in disease caused by this bacterium in patients with CDIs. Hidron *et al.* (2008) demonstrated that *E. coli* and *P. aeruginosa* are the Gram-negative organisms which are most commonly isolated from health care-associated infections; less commonly isolated organisms include *Klebsiella pneumoniae, Enterobacter* species, *Acinetobacter baumannii,* and *Klebsiella oxytoca*.

1.9.2 Opportunistic mycoses

Opportunistic mycoses affect the skin, mucosa and the internal organs and are caused by both yeast and moulds. Such infections are associated with weakness in the host's immune defences, especially as the result of long-term and severe immunosuppressed. The most important pathogenic fungi are *Candida albicans*, *Aspergillus* spp., *Cryptococcus neoformans, Cryptosporidium, Malassezia spp., and Saccharomyces cerevisiae* (Badiee and Hashemizadeh, 2014). In addition to *Candida* and other yeasts, infections can also be caused by phaeohyphomycetes and hyalohyphomycetes. These organisms act as primary infection foci, usually affecting the upper or lower respiratory tract and can spread hematogenously and lymphogenously to infect additional organs (Badiee and Hashemizadeh, 2014). At

least 70% of all human *Candida* infections are caused by *C. albicans*, and the rest by *C. parapsilosis*, *C. tropicalis*, *C. guillermondii*, *C. kruzei*. Diba *et al.* (2012) identified pathogenic fungi from the environment including: *Candida albicans*, *C. krusei*, *C. glabrata*, *C. tropicalis* and *C. parapsillosis*. Of the isolates 35(31.5%) were shown to be *Candida* species, 48(43.2%), *Aspergillus* and 28 (20.3%) of other species.

1.10 Microorganisms used throughout the following

Staphylococci aureus is a non-motile small spherical cell (1µm) found in grapelike clusters. It is a Gram- positive coccus, catalase-producing bacteria, facultative anaerobe and can be cultured on normal nutrient media at 37° C. Extracellular enzymes and exotoxins produced by this bacterium, such as coagulase, alphatoxin, leukocidin, exfoliatins, enterotoxins, and toxic shock toxin are responsible for the resultant clinical symptoms and infections. *Staphylococcus aureus* is a frequent pathogen in nosocomial infections and it causes limited outbreaks in hospitals of problems including: furuncles, food poisoning, dermatitis exfoliativa, toxic shock syndrome, carbuncles, wound infections, sinusitis, otitis media, and mastitis puerperalis (Spaulding *et al.*, 2014).

Escherichia coli is a Gram-negative, flagellated rod whose natural habitat is the intestines of animals and humans. This bacterium is a major human pathogen that causes many infections including: lower urinary tract infection such as urethritis,

cystitis, urethrocystitis; infections of the renal pelvis and kidneys (cystopyelitis, pyelonephritis), wound infections, gallbladder and bile ducts infections, peritonitis, meningitis patients. *E. coli* also causes acute urinary tract infections in 70–80% of cases and in chronic, persistent infections in 40–50% of cases, as well as about 15% of all cases of nosocomial sepsis (*S. aureus* 20%).

Candida rugosa is a budding oval yeast Branched pseudohyphae are frequently seen and occasionally septate mycelia, with chains of elongated blastoconidia. *Candida rugose*-pseudohyphae differentiates it from *C. lusitaniae*, *C. parapsilosis. Candida rugosa* has recently been cited as a possible "emerging" fungal pathogen capable of causing invasive infection in immunocompromised patients especially following the use of catheters but also via other modes of nosocomial acquisition (Pfaller, 2006). Behera *et al.* (2010) identified *Candida rugosa* as a causative pathogen of candidaemia, thirteen out of the 19 patients (68.4%) with C. rugosa candidaemia died.

1.11 Molecular biology techniques

16S rRNA and 18S rRNA analysis has been applied here to identify both bacteria and the yeasts isolates studied here. DNA can be isolated from a variety of specimens including from tissues, blood, bones, sperm, plant, hair and bacteria (Lahiri, 1992). DNA can also be used for laboratory diagnosis and in forensics (Hill *et al.*, 2000). In DNA analysis tissues or cells are first broken and the cells

are lysed using detergents or enzymes. This is followed by centrifugation to separate the DNA from other components and by DNA purification (Amann *et al.,* 1995).

1.11.1 Deoxyribonucleic acid (DNA)

Deoxyribonucleic acid (DNA) is the genetic material in living organisms. DNA plays an essential role for storing of the biological information due to its polymeric structure and because there are different nucleotides.

DNA is a polymer; a long, chainlike molecule consists of two long polynucleotide chains made up of four types of nucleotide sub-units called monomers. Each chain is called a “DNA chain” or “DNA strand”, and both chains are linked together by hydrogen bonds. The Nucleotides are composed of five carbon sugars which are linked with one or more phosphate groups and nitrogen containing base. The sugar is a deoxyribose attached with a single phosphate and one of the nitrogen bases Adenine (A), cytosine (C), guanine (G) or thymine (T). These nucleotides are attached together in a chain with the sugars and the phosphate groups form a backbone. The nucleotide subunits are linked together in a specific way that gives the DNA molecule chemical polarity. The two ends of the chain will be differing One is a hole3′ hydroxyl and the other is a knob5′ phosphate (Madigan *et al.,* 2012).

1.11.2 Polymerase Chain Reaction (PCR) technique

PCR is a powerful method of amplifying specific DNA sequences invented by Kary Mullis in 1983 (Mullis, 1990). The PCR technique used in clinical microbiology and research laboratory for identify the microbial pathogens. It used for detect pathogens which has a slow growth rate, clarify the taxonomic positions of known pathogens and help genotyping for microbial characterization which is become more specific and easily quantified between different organisms (Valones *et al.*, 2009). This technique depends on repeated synthesis of target DNA using DNA polymerase through three different steps under controlled temperatures in many thermal cycles. The steps are: **Denaturation** involves melting the double strand of the target DNA and separate them to single strands under high temperature 90-98°C for 1 minute. **Annealing** which allows the two added primers (oligodeoxyribonucletides) to anneal with the separated DNA to be amplified. The primers anneal to the opposite side of the DNA strands in their 3' end under low temperature 37-65°C for 45 seconds. In the **extension,** the DNA polymerase synthesis a new DNA strand which is complementary to the target DNA by adding the deoxynucletides (dNTPs) from the reaction mixture of the 5'-to-3' direction under optimum temperature for DNA polymerase 75–80°C for 2 minutes. These steps run in a single cycle so many cycles are needed to amplify the specific DNA to millions of copies. PCR reaction set of 30 cycles. Final elongation: this step is optional and requires a temperature of 70-74°C for 5-15 minutes after the final step of PCR to ensure that all single strand of DNA is elongated completely. Final

hold: in this step, the reaction mixture is cooled at 4-15°C for a short time to allow the products to be stored.

The aim of the work described here was to:

1) Studies the distribution of bacteria in the environment and their survival in the healthcare settings including: sinks, lift buttons, computer keyboards and computer mice, mobile telephones, mirrors in toilets, dust obtained from vacuum cleaners, under the surfaces of shoes, books and shelves in libraries and upper surfaces of water taps.
2) Determine of the number of bacteria on hands after washing and drying normally and with warm air dryer and quantify of bacteria transferred from hand warm air dryers
3) Determine the factors which influence the survival of bacteria and to a lesser extent *Candida* in the built environment on ceramic tiles, on copper and plastic plumbing surfaces, and on new toothbrushes.
4) Isolation pathogenic bacteria from used toothbrushes and determine the effect of toothpastes on growth of pathogenic bacteria.
5) Determine of effectiveness of antibacterial cloths in inhibiting the growth of bacteria and yeast.
6) Determine the survival and relevant metabolic diversity of bacterial isolates.

CHAPTER 2

THE DISTRIBUTION OF BACTERIA IN THE ENVIRONMENT AND THEIR SURVIVAL IN HEALTHCARE SETTINGS

2.1. Isolation of bacteria from sinks, toilets and other medical environments

Hospitals and other health care settings act as an obvious potential reservoir for pathogens (Dancer, 2009). (Bauer *et al.*, 1990, Kayabas *et al.*, 2008, Medina *et al.*, 1997, Sehulster *et al.*, 2003). Contaminated hand washing sinks are an obvious source of infection, especially where they are used for disposing of body fluids, where they become a focus for the survival of pathogens and especially biofilms; surprisingly perhaps, healthcare workers can become contaminated when washing their hands in a contaminated sink (Roux *et. al.*, 2013).

2.2. Isolation of bacteria from sinks

2.2.1. Materials and Methods

1) Isolation of samples and collection

Sterile cotton swabs wetted by dipping in normal saline were used to collect samples from sinks. All samples were labelled and streaked on Nutrient Agar (Oxoid) plates, followed by incubation at 25ºC under aerobic conditions for 24hrs. After incubation the colonies were identified. The sinks examined were located as follows: Sheffield University: Firth Court Building, Disability and dyslexia support service, The Alfred Denny Building, Information Commons Building,

Students Union Building. Other areas in Sheffield: Sheffield Train Station, local supermarket, local hospital, various private dwellings.

2) Purification of isolates

All samples were isolated from sinks and then streaked on media in Petri dishes. The main medium used was Nutrient Agar, incubation was then at 37°C for 48 hours. The isolates were purified to single colonies and subjected to molecular identification.

3) Identification of bacterial isolates using 16s rRNA technique

A bacterial suspension in LB medium was prepared and incubated overnight at 37ºC. After the incubation period, 1-3 ml of media was transferred to a sterile Eppendorf tube and centrifuged at 6000xg for 2 min at room temperature and the supernatant was decanted completely. A KeyPrep bacterial DNA extraction kit supplied by ANACHEM® was used and all steps were conducted as described in the instructions provided by the Company. Buffer (100µl) R1 was added to the pellet and the cells were re-suspended completely by pipetting up and down. After full cell homogenising, 20 µl of lysosyme was added, mixed and incubated at 37^0 C for 20 min. The mixture was then digested by centrifugation at 10,000xg for 3 min and the supernatant was completely decanted. The pellet was then re-suspended in 180 µl of buffer R2 and 20 µl of proteinase K was added and incubated at 65^0 C for 20 min in a water bath with occasional mixing every 5 min.

400 µl of buffer. BG was added and mixed thoroughly by inverting the tube several times until a homogeneous solution was obtained and then incubated for 10 min at 65^0 C. After the incubation period, 200 µl of absolute ethanol was added and mixed thoroughly.

The sample was next transferred into a column assembled in a clean collection tube and centrifuged at 10,000 xg for 1 min while the flow was discarded. The column was washed by addition of 750 µl of wash buffer and centrifuged at 10,000 xg for 1 min while the flow was discarded. Finally, the column was placed in a clean micro-centrifuge tube and 70µl of elution buffer was added and centrifuged at 10,000xg for 2 min to elute DNA. DNA was stored at -20^0C until the next step.

4) Gel electrophoresis

Gel electrophoresis was conducted to ensure that the bacterial DNA was well-extracted and purified. The following steps were used.

4.1 Agarose preparation

Powdered agarose was weighed carefully (0.5 g) into a conical flask and 50 ml of 1x TAE (Tris Acetate EDTA) buffer was added with 40ml of distilled water. The contents of the flask were then mixed and placed in a microwave plate until the contents just began to boil and all the powdered agarose is melted. After the contents cooled to 50-55 °C, ethidium bromide solution was added to give a final concentration of 5 pg/mL. The mixture was then be poured into a gel tray and left

to solidify. The gel was finally placed in an electrophoresis tank and submerged in 1x TAE buffer to ensure that the sample diffused into the wells.

4.2 Sample loading

DNA samples (10 µl) were prepared by the addition of 5X (2µl) loading dye (blue or orange) to the samples and loaded into the wells of the gel. All samples were loaded at the same time. 6 µl of hyper ladder was then added into an adjacent well as a reference. The voltage was set to the desired level at 80V for 40 minutes to initiate electrophoresis. The leads were then attached allowing DNA to migrate within the gel toward the anode. After electrophoresis the gel was removed from try, and the DNA fragment was viewed on a UV transilluminator; images were then captured using a connected digital camera.

4.3. Sample amplification

The Polymerase Chain Reaction (PCR) technique was used. A mixture in a sterile Eppendorf tube was prepared as follows: 12 µl of master mix, 1 µl of forward primer, 1 µl of reverse primer, 1 µl of the DNA sample, and 35 µl of sterile distilled water. The mixture was inserted in a PCR machine and the programme was adjusted as follows:

Table 2.1 The Polymerase Chain Reaction (PCR) cycle.

Steps	Temperature	Time (Min)	Number of cycles
Initialization (Initial denature)	94°C	3	1
Denature	94°C	1	35
Annealing	60°C	1	35
Extension/Elongation	72°C	1	35
Final elongation	72°C	5	1
Hold	4°C		1

5) 16S rRNA sequencing and phylogenetic analysis

After PCR, aliquots of 10 µl of each sample were allowed with 1µl of forward primer and 1µl of reverse primer in a sterile small size tube and sent to the Medical School Core Genetics Unit (University of Sheffield) to be sequenced. 16S rRNA gene sequences were adapted using the Finch TV software and then exported into the Basic Local Alignment Search Tool (BLAST), available from the website of the National Centre for Biotechnology Information (NCBI), to identify matches with existing characterized reference sequences. Partial sequences, generated in this experiment, were assembled and the errors of

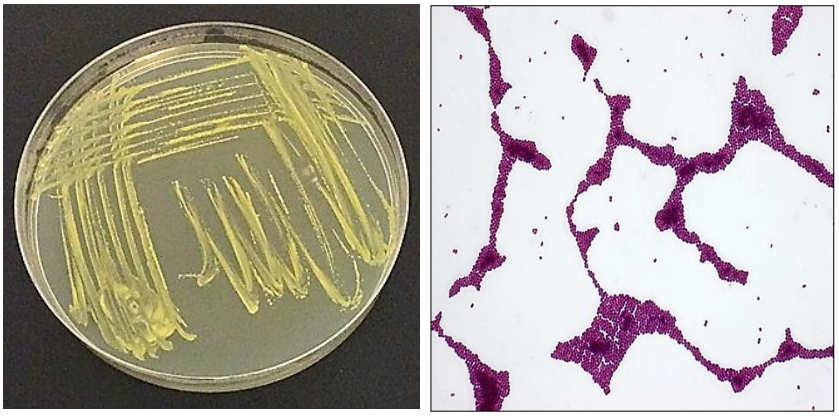
consensus sequences were corrected manually by using Finch TV software (version 1.4). In Finch TV software, the unknown nucleotide is represented as N, and it could be either A, or T, or G, or C, according to the different colours which appear (Mishra *et al*., 2010).

2.2.2. Results

1) Isolation of bacteria from various sinks by cultivation on Nutrient Agar medium

Bacteria were isolated using Nutrient Agar which facilitates the rapid isolation of bacteria from mixed cultures and used for biochemical or serological tests. This medium is a basic culture medium used for maintaining microorganisms, cultivating fastidious organisms by enriching with serum or blood and are also used for purity checking prior to biochemical or serological testing. The presence of peptic digest of animal tissue, beef extract and yeast extract provides the necessary nitrogen compounds, carbon, vitamins and also some trace ingredients necessary for the growth of bacteria; sodium chloride maintains the osmotic equilibrium of the medium. The following bacteria were isolated from the surface of ceramic sinks.

2) Light microscope images. The isolates were examined under a light microscope (Figure 2.1) in order to confirm that they were bacteria

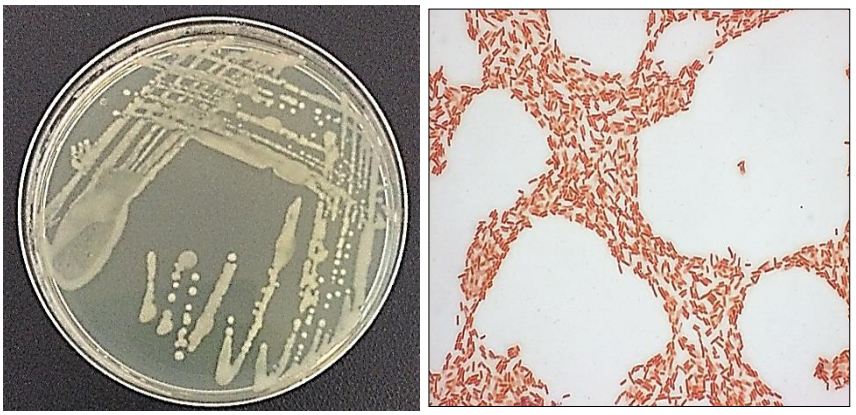


Kocuria rhizophila

Gram stained. Magnification: 100x.

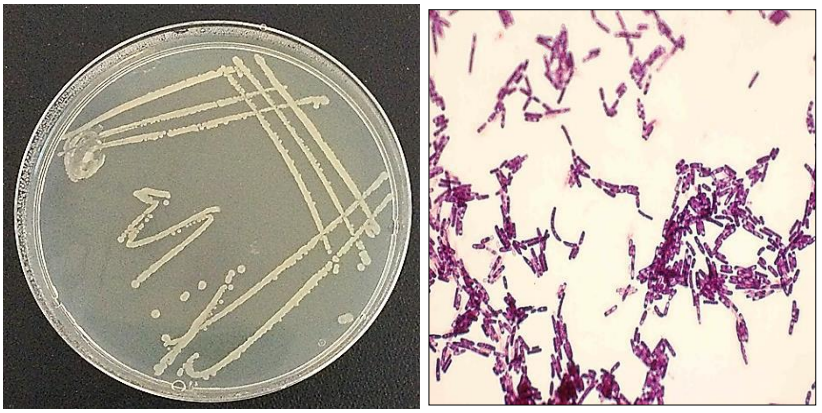
Micrococcaceae Bacterium

Gram stained. Magnification: 100x.



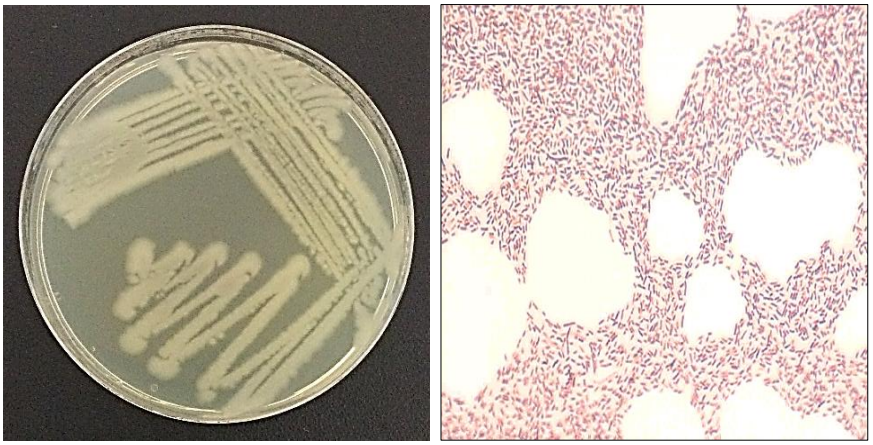
Klebsiella oxytoca

Gram stained. Magnification: 100x.



Bacillus subtilis

Gram stained. Magnification: 100x.



Bacillus cereus

Gram stained. Magnification: 100x.

Figure 2.1: Nutrient Agar plates showing cultured bacteria isolated from various sinks, also microscopy images shows the bacteria under the light microscope.

Table 2.2: Bacteria isolated from various sinks.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
S1	*Klebsiella oxytoca*	100%	CP011618.1
S2	*Bacillus subtilis*	100%	KP340123.1
S4	*Kocuria rhizophila*	99%	KM978822.1
S5	*Bacillus cereus*	99%	KC731425.1
S6	*Micrococcus luteus*	99%	KT339390.1

2.2.3. Discussion

The bacteria shown in Table 2.2 were isolated from chosen sinks which are in general use and so represent the environments typical of health care settings. Five bacteria were isolated and identified, two of which were species of *Bacillus*.

Klebsiella oxytoca

Klebsiella is commonly isolated in the clinical laboratory from specimens of blood, urine and respiratory secretions. *Klebsiella* are non-motile, Gram-negative bacilli, glucose fermenters, and form red colonies on MacConkey agar; negative results for cytochrome oxidase activity, hydrogen sulfide production in triple sugar iron agar, arginine and ornithine, decarboxylation, phenylalanine deamination, and citrate utilization. *Klebsiella oxytoca* is a diazotroph, which colonises plants and

fixes atmospheric nitrogen in, for example, the barley rhizosphere. This organism causes colitis and sepsis (Hogenauer *et al*., 2006).

Bacillus cereus

B. cereus group are Gram-positive, rod-shaped, spore formers, motile. *Bacillus cereus* is the most frequently isolated of *Bacillus* spp involved in nosocomial infections. It has been described an outbreak of invasive *B. cereus* infections in neonatal intensive care units. Kalpoe *et al* (2008) reported an outbreak of vancomycin resistant *B. cereus* respiratory tract colonization in patients in pediatric intensive care units. *Bacillus cereus* is also common in bloodstream infections in patients with hematologic malignancies due to contamination of re-used towels. *Bacillus cereus* is a highly important eye pathogen because it can cause blindness rapidly; endophthalmitis associated with this bacterium often results in significant vision impairment. This bacterium is the most known food-borne pathogen associated with food-poisoning. It has also been found to be associated with fulminant pneumonia in immunocompetent patients and with oral diseases; meningoencephalitis and meningitis in infants, neonates and immunocompromised individuals; necrotizing fasciitis and myositis (Liu, 2011).

Bacillus subtilis

Bacillus species, including *B. subtilis*, can form endospores which allow them to survive heat treatment and disinfection procedures and as a result, present serious health problems as contaminants of food or in the general hospital settings as a cause of nosocomial infections, especially in immunocompromised patients. These bacteria produce toxins which have been linked as the causative agent of several human diseases including endophthalmitis, inflammation of intraocular tissues or fluids due to intraocular infection (Liu, 2011). They also contribute to foodborne infections by producing toxins with a cereulide-like mode of action (e.g. in oral disease, mainly gingivitis and periodontitis). Cryptic pyogenic infections of the central nervous system (CNS) following dental affections have also been implicated to *B. subtilis* and *B. circulans* (Liu, 2011).

Kocuria rhizophila

Kocuria rhizophila cells are Gram- positive, non-acid-fast, non-motile, non-endospore forming, aerobic, and occur in pairs, tetrads, and packets. *Kocuria rhizophila* is widely distributed in the natural environments such as soil, the rhizosphere, freshwater, marine sediments, and fermented foods. *Kocuria* spp are also found in the skin, mucosae, and oropharynx of humans as commensals, although several of them have been associated with human diseases (Liu, 2011). Becker *et al.*, (2008) reported a case of *Kocuria rhizophila* infection in a boy with methylmalonic aciduria. The patient developed sepsis and showed symptoms of

acute pancreatitis and fever. A *Kocuria rhizophila* strain was also isolated from blood samples drawn through a port system and from peripheral veins during septic episodes. A number of *Kocuria* species are opportunistic human pathogens associated with catheter-related bacteraemia, pneumonia, intracranial abscesses, septic arthritis, meningitis, peritonitis, and endocarditis in immunocompromised patients (Liu, 2011).

Micrococcus luteus

Members of the genus *Micrococcus* are Gram-positive cocci, aerobic, non-motile, and non-endospore forming. *Micrococcus* spp. are commonly found as members of the normal skin flora of humans and other mammals. *Micrococcus* strains such as *M. luteus* are opportunistic human pathogens associated with catheter-related bacteraemia in patients undergoing heamodialysis or leukaemia treatment, pneumonia, endocarditis patients particularly immunocompromised individuals, intracranial abscesses, continuous ambulatory dialysis peritonitis, septic arthritis, and meningitis (Liu, 2011).

The results show that sinks are clearly a potential source of pathogens, both in the domestic and healthcare settings.

Hospital sinks are considered to be one of the most frequently implicated reservoirs for MDR Gram-negative bacilli, including MDR coliforms (Roux *et al.*, 2013). *K. pneumoniae* strains which have the ability to survive for long periods

within plumbing components are also more likely to contain bacteria exhibiting extended-spectrum β-lactamases (Yang and Zhang, 2008). Removal and replacement of the sink and associated pipe work together with upgrading practices for sink use and cleaning is often required to end an outbreak. Outbreaks of MDR *Klebsiella* are also often associated with the bad practise of tipping patient fluids down the nearest available sink instead of removing clinical waste to the designated waste sluice located at a distance (Roux *et al.,* 2013). Not surprisingly, lower rates of sink contamination are significantly linked to daily bleach disinfection, in addition to restrictions being placed on sink use for hand washing only and not the routine disposal of fluid or clinical waste (Roux *et al.,* 2013, Yang and Zhang, 2008). It is noteworthy in the finding reported in this Thesis that the bacteria isolated from sinks were essentially environmental species and not those capable of causing major life-threatening infections. It needs to be emphasised, however, that even these bacteria can cause major problems in immunocompromised patients.

2.3 Isolation of bacteria from lift buttons surfaces

2.3.1 Methods

Sterile cotton swabs wetted by dipping in normal saline were used to collect samples from environmental surfaces such as lifts buttons from different floors in the MBB building and Sheffield University Students' Union. All samples were labelled and streaked on to Nutrient Agar Plates which were incubated at 25ºC

under aerobic conditions for 24hrs. After incubation, the colonies were identified. Genomic DNA was extracted from each isolate and was identified using 16S rRNA. The extraction of genomic DNA was by using KeyPrep bacterial DNA extraction kit (supplied by ANACHEM). The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

2.3.2 Results and Discussion

1) Isolation of bacteria from various lift buttons by cultivation on Nutrient Agar medium

Bacteria were cultured using Nutrient Agar having been isolated from lift buttons. The bacteria shown in (Figure 2.2)

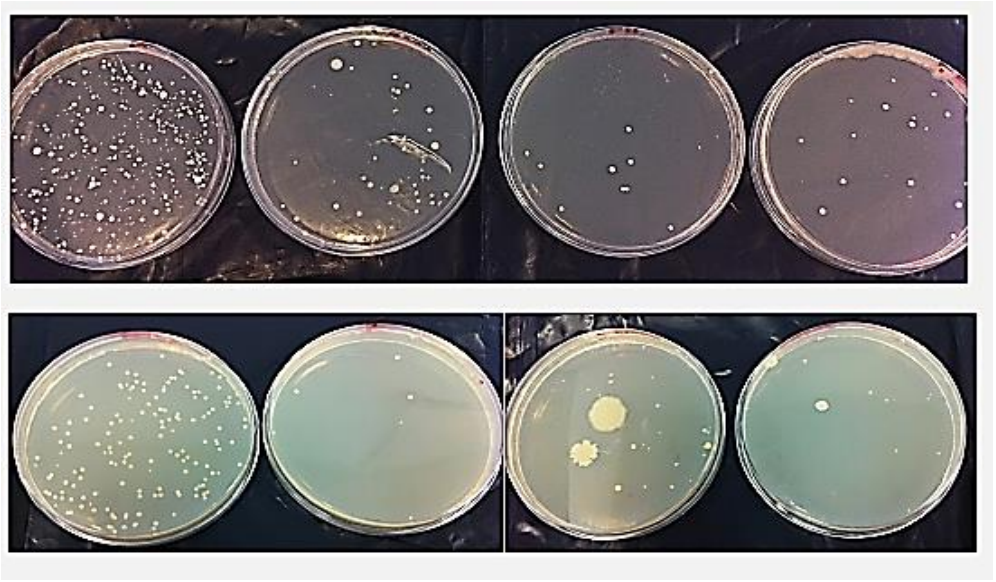


Figure 2.2: Bacteria contaminating lift buttons. From left to right, shows ground floor to upper floors from various locations.

Table 2.3: Bacteria isolated bacteria from lift buttons.

Representative sequence	Closest matches identification	Sequence identity	NCBI (Accession number)
6W3	*Staphylococcus warneri* BCL-34	99%	KT582294.1
7W1	*Staphylococcus epidermidis*	98%	FR797804.1
7Y3	*Micrococcus luteus* MBS022	99%	KM378607.1

Staphylococcus

The characteristics of these bacteria include:

Staphylococcus is a genus of catalase positive Gram-positive bacteria. *Staphylococcus* bacteria appear as round (cocci) and come together as grape-like clusters. *Staphylococci* consist of >40 species and are noted for their ability to cause disease, with *Staphylococcus aureus* being a most common pathogen of man and animals. Most *Staphylococcus* species are however, harmless and normally live on the skin and mucous membranes of humans and other organisms (Liu, 2011).

Staphylococcus aureus is mainly a commensal organism residing on the human epithelia of the mucosae and skin. It has its primary ecological site in the vestibulum nasi, located in the forefront region of the nose. None-nasal sites typically harbouring the organism include the skin, perineum, and pharynx; other

sites include the gastrointestinal tract, vaginas, and axillae. This bacterium causes superficial skin lesions like impetigo, styes and furuncules, cellulitis folliculitis, carbuncles, staphylococcal scalded skin syndrome (SSSS), and abscesses (Liu, 2011). More serious infections include pneumonia, mastitis, phlebitis, meningitis, urinary tract infections (UTIs), and septicaemia. *Staphylococcus aureus* infections including osteomyelitis, hospital-acquired (nosocomial) infections in surgical wounds and infections associated with indwelling medical devices. *S. aureus* also causes food poisoning by producing enterotoxins and toxic shock syndrome (TSS) by release of superantigens into the blood stream (Liu, 2011).

Staphylococcus epidermidis is a skin commensal which can be isolated from mucous membranes, such as the groin or axilla, exposed skin surfaces and saliva. It is the main human pathogen in intravascular catheter-related infections, nosocomial bacteraemia, endocarditis, urinary tract and surgical wounds infections and infections of the central nervous system, ophthalmologic infections, peritoneal dialysis-related infections and infections of prosthetic joints (Liu, 2011). Some isolates produce slime or biofilm which is the major virulence factor of *S. epidermidis*, enabling colonization and persistence on prosthetic material, the resistance to the effects of antibiotics, and the ability to evade the immune system (Liu, 2011).

Micrococcus are Gram-positive, non-motile, non-endospore forming, aerobic cocci. *Micrococcus luteus* have been associated with catheter-related bacteraemia in patients undergoing haemodialysis or leukaemia treatment, pneumonia,

endocarditis, intracranial abscesses, continuous ambulatory dialysis peritonitis, septic arthritis, and meningitis (Liu, 2011).

The number observation of bacterial contamination of lift buttons decreased from ground floor towards upper floors as shown in Figure 2.2. These results agree with the findings of Al-Ghamdi *et al.* (2011) who showed that the average rate of bacterial contamination of different objects within the hospital environment was 95.5% with elevator buttons showing the highest percentage (97%). Scott and Bloomfield (1990) suggested that when contaminated surfaces are contacted with the fingers, a significant number of organisms can be transferred which can be subsequently recovered on an agar surface. Inanimate objects can play a role in the transmission of human pathogens. These surfaces have been shown to carry both non-pathogenic and pathogenic bacteria and even a single hand contact with a contaminated surface results in a variable degree of pathogen transfer.

2.4 Isolation of bacteria from computer keyboards and computer mice

Multidrug-resistant strains of *S. aureus*, particularly methicillin resistant *S. aureus* (MRSA), present a major clinical and epidemiological problem in healthcare settings as they are easily transferred among hospital staff and patients, especially in intensive care units (ICUs). Hails *et al.* (2003) found that at least 16% of patients were colonised with MRSA. A significant factor contributing to the transmission of microorganisms is their ability to survive on environmental

surfaces. Also the microbial contamination of environmental surfaces in the hospital may contribute to the spread of potential pathogens without direct patient contact. Coagulase-negative Staphylococci have been cultured from all keyboards investigated in different studies conducted in the USA (Anastasiades *et al.*, 2009). In another study which focused on the isolation of MRSA, 65% of nurses, who had contact with MRSA-infected patients, bacteria contaminated their uniforms as well as the keyboards and computer mice (CM) in the hospital wards. These results confirmed that inanimate objects can serve as reservoirs for bacteria. Hartmann *et al.* (2004) also found that keyboards and CM might serve as a source for the transmission of microorganisms.

In a study investigating the presence of both Gram-positive and Gram-negative bacteria on computer keyboards, coagulase-negative staphylococci and *S. aureus* were isolated from 100% and 4% of keyboards, respectively (Rutala *et al.*, 2006). It was suggested that the use of plastic keyboard covers could reduce contamination. It was then recommended that the same infection prevention measures employed during direct contact with patients (i.e. hand washing and use of gloves), should be enforced when handling computer hardware in healthcare settings.

As has been mentioned in Chapter 1, medical surfaces present a major source of outbreaks of community-acquired and nosocomial infections. Such surfaces include frequently used computer keyboards and accompanying mice which

harbour skin and dust bacteria, such as species of *Staphylococcus* and *Streptococcus epidermidis* and fungi (yeasts), notably *Candida albicans*. Keyboards were also implicated in burns unit-associated nosocomial infections by *A. baumannii* (Neely *et al.*, 1999) MRSA and *Enterobacter* spp. (Bures *et al.*, 2000; Goldman, 2000). It goes without saying that hospital keyboards and computer mice should be routinely cleaned and covered with transparent plastic covers when not in use. Hand hygiene is also necessary to avoid cross contamination of keyboards and other computing devices. This is especially important since contaminated personal computers are often contaminated with Staphylococci and *Pseudomonas* spp. And can transmit MRSA (Isaacs *et al.*, 1998).

2.4.1 Materials and Methods

All samples are isolated from computer keyboards using swabs (70 samples) streaked on petri dishes containing Nutrient Agar and incubated at 25°C for 48 hours. Genomic DNA extracted from each isolate was identified using 16S rRNA. The extraction of genomic DNA by using (KeyPrep bacterial DNA extraction kit supplied by ANACHEM), The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

2.4.2 Results

1) Isolation of bacteria from computer keyboard

Bacteria were cultured using Nutrient Agar after isolation from computer keyboards and mice.

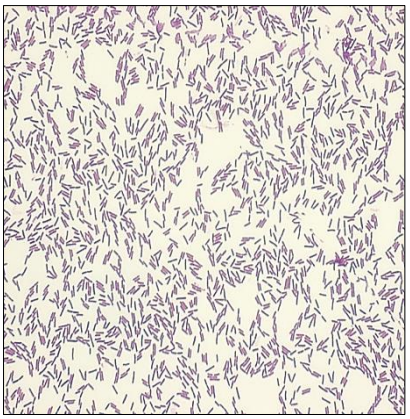
2) Light microscope images. The isolates were examined under a light microscope (Figure 2.3).

Bacillus amyloliquefaciens

Gram stained. Magnification: 100x.

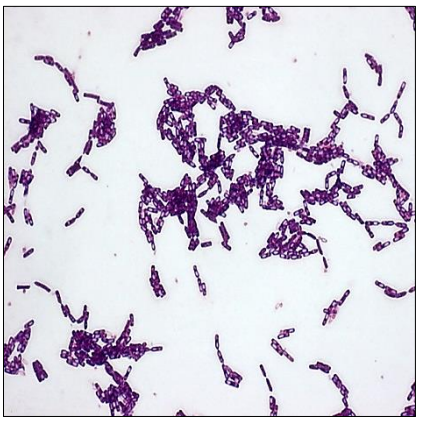
Bacillus subtilis

Gram stained. Magnification: 100x.

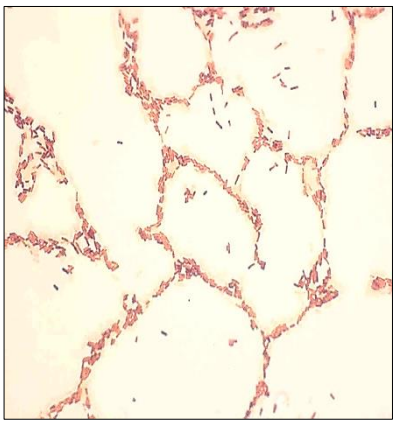
Brevibacillus brostelensis

Gram stained. Magnification: 100x.

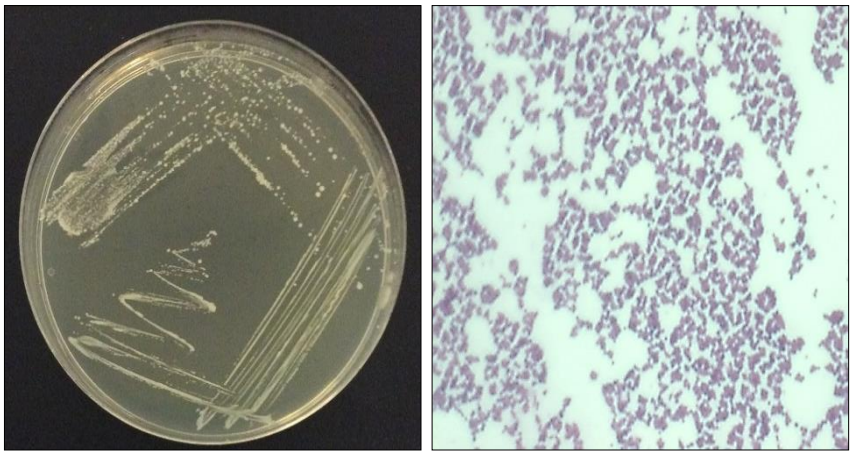
Bacillus cereus

Gram stained. Magnification: 100x.

Pantoea caldia

Gram stained. Magnification: 100x.



Staphylococcus epidermidis

Gram stained. Magnification: 100x.

Figure 2.3: Nutrient Agar plates showing cultured bacteria isolated from various computer keyboards, also microscopy images showing the bacteria under the light microscope.

Table 2.4 Bacteria isolated from various computer keyboards.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
KB1	*Bacillus subtilis*	99%	KJ746466.1
KB4	*Bacillus amyloliquefaciens*	99%	AB301004.1
KB6	*Brevibacillus brostelensis*	98%	EU816699.1
KB11	*Staphylococcus epidermidis*	99%	KF575163.1
KB13	*Pantoea caldia*	99%	AB907785.1
KB14	*Bacillus cereus*	99%	DQ923480.1
KB21	*Pseudomonas luteola*	99%	KC429633.1

Bacillus amyloliquefaciens

This bacterium typically presents as motile, Gram-positive rods, often forming chains, with peritrichous flagella. Optimal temperature for growth is 30 to 40°C, while no growth occurs below 15°C or above 50°C. *B. amyloliquefaciens* can be isolated from soil and brackish sediments (Priest *et al.,* 1987). *B. amyloliquefaciens* is not known to produce any mammalian toxins, and is not associated with food-borne disease. No problems have been reported, and none are expected from exposure to *B. amyloliquefaciens* via drinking water (Priest *et al*., 1987).

Brevibacillus brostelensis

Brevibacillus brostelensis cells present as Gram-positive rods, motile with peritrichous flagella. It is a thermophilic, spore-forming rod with a growth optimum at 50°C. Colonies are flat, smooth, circular, and entire. This bacterium produces a soluble brown-red pigment(s) on nutrient agar and is strictly aerobic. The habitat of *Brevibacillus* overlaps with that of *Bacillus* and is associated with soils and dairy environments (Sanders, 2003; Shida *et al*., 1995).

Pseudomonas luteola

Pseudomonads appear as straight or slightly curved Gram-negative rods. They are usually easily differentiated from Enterobacteriaceae by a lack of a bipolar

staining. Isolates often seen as clusters of rods encapsulated in a thick pink staining alginate coat. *Pseudomonas* spp. grow on several different nonselective agars, including nutrient, 5% blood, chocolate, and MacConkey agars (Liu, 2011). Most species are aerobic and grow at 37°C, and within 24h, form visible colonies. This bacterium is oxidase negative and produces a non-diffusible yellow pigment. P*seudomonas* spp. act as opportunistic pathogens and *P. luteola* can cause community- or hospital acquired infection in humans especially patients in an intensive care unit. *Pseudomonas luteola* causes dialysis associated peritonitis; cellulitis; sepsis; prosthetic valve endocarditis; and postoperative endophthalmitis (Liu, 2011).

Pantoea calida

Pantoea calida cells are Gram-negative rods that are facultatively anaerobic and motile. Colonies are non-pigmented and convex, oxidase-negative and catalase-positive (Fritz *et al.*, 2014). *Pantoea calida*, a recently described environmental Enterobacteriaceae organism, has yet to be associated with human infection, although Fritz *et al*., (2014) isolated this organism from a patient with postoperative meningitis.

2.5. Isolation of bacteria from mobile telephones

2.5.1 Materials and Methods

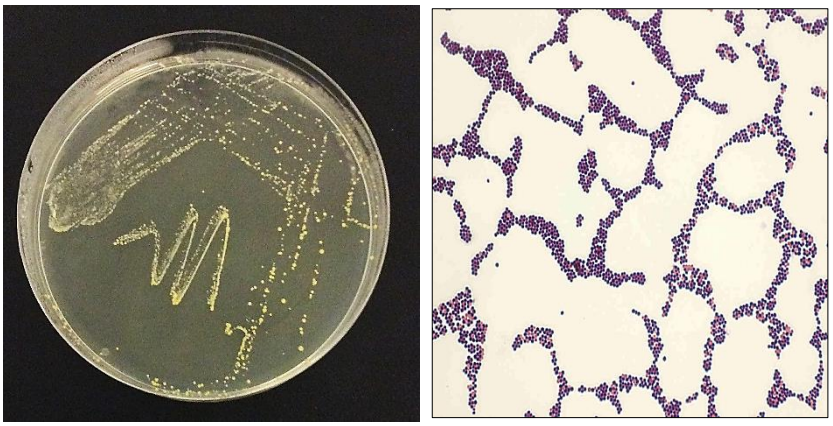
Isolates were obtained from a variety of mobile telephones (30 samples) using nutrient agar medium. Incubation was at 37°C for 48 hours and the isolates were identified using 16S rRNA. Extraction of genomic DNA was by using Norgen's Fungi/Yeast Genomic DNA Isolation Kit. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

2.5.2 Results

1) Isolation of bacteria from mobile phones

Bacteria were cultured using Nutrient Agar after isolation from mobile phones.

2) Light microscope images. The isolates were examined under a light microscope (Figure 2.4).

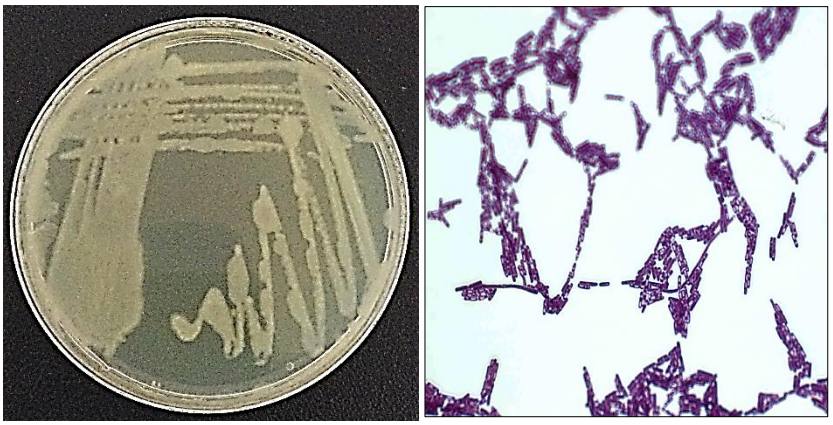


Staphylococcus epidermidis

Gram stained. Magnification: 100x.

Staphylococcus warneri

Gram stained. Magnification: 100x.



Bacillus cereus

Gram stained. Magnification: 100x.

Bacillus subtilis

Gram stained. Magnification: 100x.

Figure 2.4: Nutrient Agar plates showing cultured bacteria isolated from various mobile phones, and also microscopy images showing the bacteria under the light microscope.

2) Table 2.5: Bacteria isolated from various mobile phones.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
3P	*Staphylococcus epidermidis*	99%	KJ398217.1
15P1	*Staphylococcus warneri*	99%	KP771665.1
15P2	*Bacillus subtilis*	99%	HG764646.1
18P	*Bacillus cereus*	99%	KJ612539.1

Staphylococcus warneri a Gram-positive member of the microbiota, normally found on the skin of humans and animals. *S. warneri* is a significant opportunistic nosocomial pathogen causing complications to the use of central venous catheters, prosthetic heart valves and joints, and neurosurgical ventricular shunts (Incani *et al.*, 2010). *Staphylococcus warneri* has been associated with bacteraemia in hospitalized patients; with intravascular catheter infections in immunocompromised patients (Incani *et al.*, 2010).

2.6 Isolation of bacteria from mirrors in toilets

2.6.1 Materials and Methods

Isolates were obtained from a variety of toilet mirror surfaces (30 samples) using Nutrient Agar medium. Incubation was at 25°C for 48 hours and the isolates were

identified using 16S rRNA. Extraction of genomic DNA was by using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

2.6.2 Results

1) Isolation of bacteria from mirrors

Bacteria were cultured using Nutrient Agar after isolation from mirror surfaces.

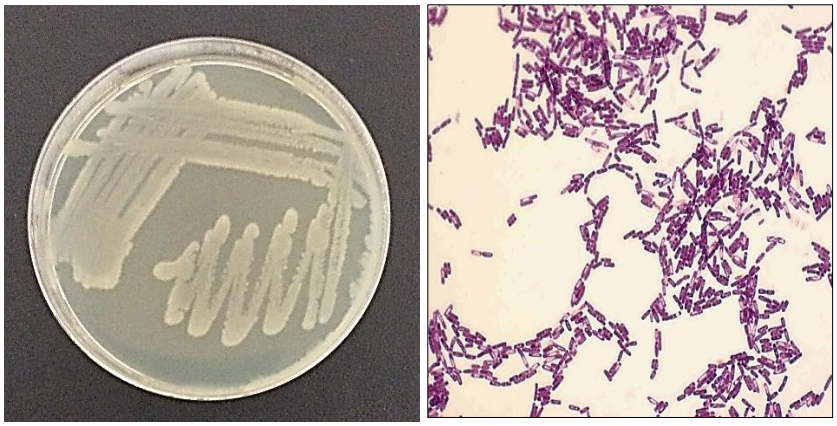
2) Light Microscope images. The isolates were examined under a light microscope (Figure 2.5).

Bacillus cereus KP100400.1

Gram stained. Magnification: 100x.

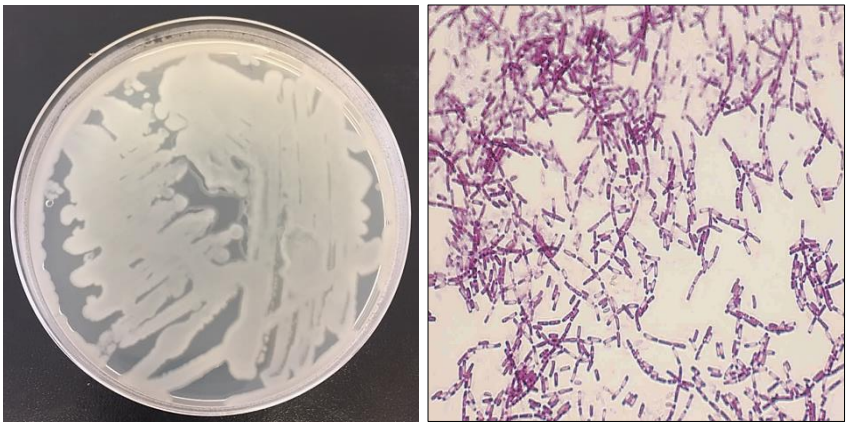
Staphylococcus haemolyticus

Gram stained. Magnification: 100x.



Bacillus cereus Q659737.1

Gram stained. Magnification: 100x.



Bacillus subtilis DQ683077.1

Gram stained. Magnification: 100x.

Figure 2.5: Nutrient Agar plates showing cultured bacteria isolated from various mirror surfaces, and also microscopy images showing the bacteria under the light microscope.

Table 2.6: Bacteria isolated from mirrors.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
M8-8	*Bacillus cereus*	99%	KP100400.1
M6-1	*Bacillus subtilis*	99%	DQ683077.1
M15-1	*Bacillus cereus*	99%	JQ659737.1
M14-1	*Staphylococcus haemolyticus*	99%	KC139455.1

Staphylococcus haemolyticus is a major cause of human disease in humans and has been implicated in native valve endocarditis (NVE), septicaemia, urinary tract infections, peritonitis, and wound, bone, and joint infections. It forms biofilms which allow it to colonize and persist on prosthetic material where it shows resistance to antibiotics and is able to evade the immune system (Liu, 2011).

2.7 Isolation of bacteria from vacuum cleaner dust samples obtained from carpets, textiles and upholstered furniture

2.7.1 Materials and methods

Dust samples were obtained from a variety of different vacuum cleaners (30 samples) for use in determining the bacterial content of the waste. The dust was placed on the surface of Nutrient Agar medium plates (NA) and then incubated at 25°C for 3 to 5 days. Extraction of genomic DNA was achieved using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

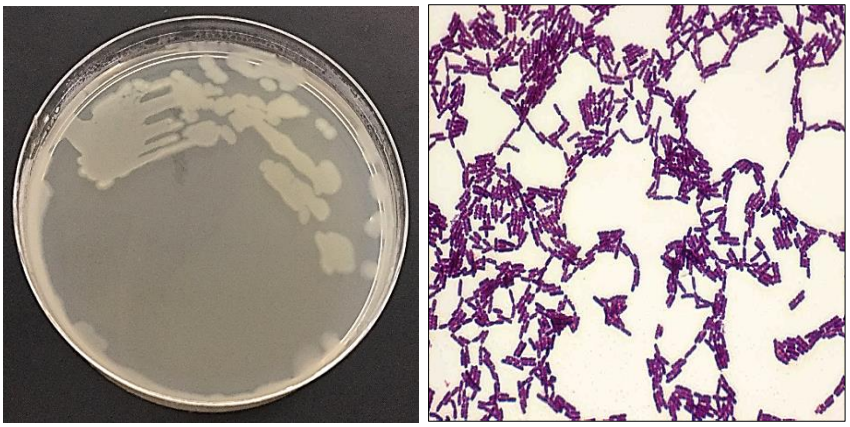
2.7.2 Results and Discussion

1) Isolation of bacteria from dust samples of various vacuum cleaners

Bacteria were cultured using Nutrient Agar which isolated from dust samples.

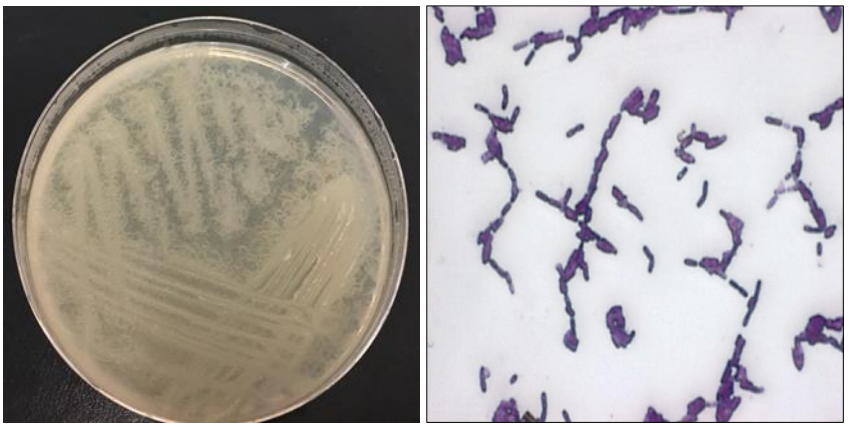
2) Light microscope images

In order to confirm that they were bacteria, the isolates were examined under a light microscope (Figure 2.6).



Bacillus thuringiensis FJ174596.1

Gram stained. Magnification: 100x.

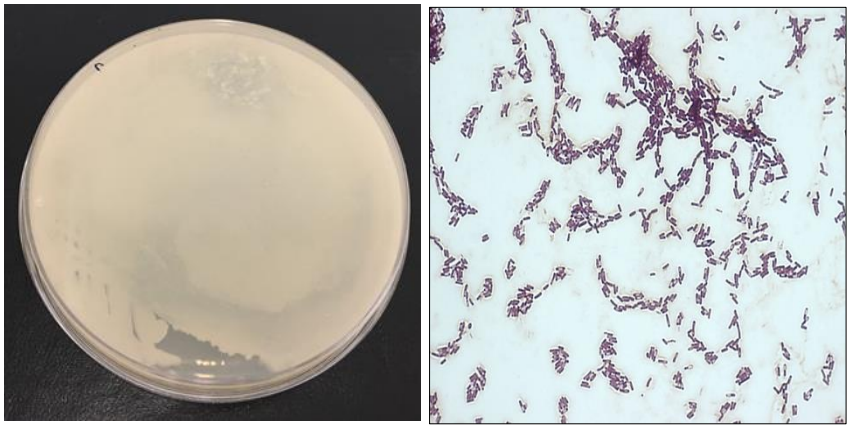


Bacillus mycoides KR088435.1

Gram stained. Magnification: 100x.

Bacillus licheniformis DQ071560.1

Gram stained. Magnification: 100x.



Bacillus subtilis KF220577.1

Gram stained. Magnification: 100x.

Figure 2.6: Nutrient Agar plates showing cultured bacteria isolated from dust samples of various vacuum cleaners, and also microscopy images showing the bacteria under the light microscope.

Table 2.7: Bacteria isolated from dust samples of various vacuum cleaners.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
VC1	*Bacillus thuringiensis*	98%	FJ174596.1
VC2	*Bacillus mycoides*	99%	KR088435.1
VC3	*Bacillus licheniformis*	99%	DQ071560.1
VC4	*Bacillus subtilis*	98%	KF220577.1

Bacillus licheniformis

B. licheniformis has been shown to be the cause of bacteremic episodes in patients having hemotological malignancies. Only one case has been reported of *B. licheniformis* nosocomial infection in neonates. In immunocompetent individuals, *B. licheniformis* bacteraemia has been reported in association with central venous catheters and with peritonitis in patients undergoing peritoneal dialysis (Liu, 2011). *B. licheniformis* has also been shown to be involved in foodborne illnesses due to its ability to produce toxins with a cereulide-action mode. Infections caused by this bacterium include, ophthalmitis, septicaemia, bacteraemia, and peritonitis. *Bacillus licheniformis* was isolated from patients suffering from eye trauma, lymphoma, leukaemia and metastatic lung cancer (Liu, 2011).

Bacillus thuringiensis

Bacillus thuringiensis is an insect pathogen widely used as a biopesticide. Kuroki *et al.* (2009) demonstrated *B. thuringiensis* species can form biofilms in nosocomial bacteraemia due to catheter infection. There is also a report of fatal *B. thuringiensis* bacteraemia in a neutropenic patient suffering from severe pulmonary disease showing that this entomopathogenic bacterium may be an opportunistic pathogen in immunocompromised patients; it is also the causative agents of infectious endophthalmitis and oral diseases, particularly gingivitis and periodontitis (Kuroki *et al.*, 2009).

Bacillus mycoides

Bacillus mycoides is typically isolated from soil and plant rhizosphere but has also been shown to be a causative agent of infectious endophthalmitis (Liu, 2011).

2.8 Isolation of bacteria from soles of shoes

An obvious potential infection hazard is presented by the transfer of microorganisms from the soles of shoes to floors and other surfaces within health care environments and pathogens can be carried in this way from environmental sources, notably soils and cat and dog faeces. In order to prevent the contamination, shoe-cover-alls should be provided for all persons entering

sensitive medical areas, such as where immunocompromised patients are being treated.

2.8 Isolation of bacteria from the under surface of shoes

2.8.1 Materials and Methods

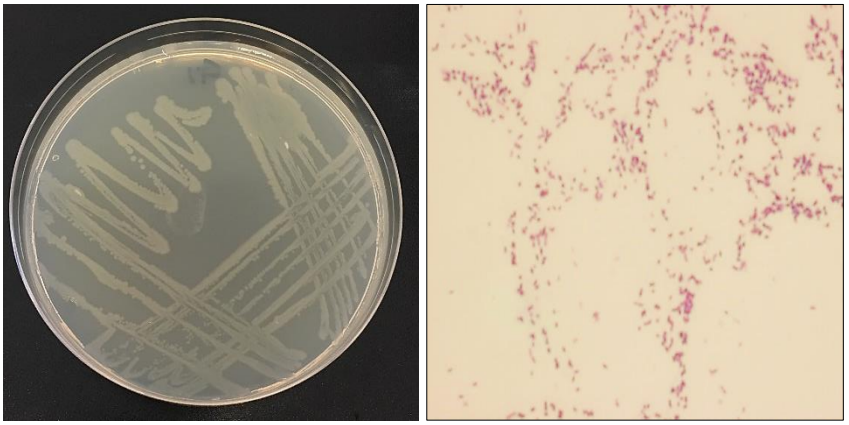
Isolates were obtained from a variety of shoe surfaces (30 samples) using Nutrient Agar medium; incubation was at 37°C for 48 hours and the isolates were identified using 16S rRNA. Extraction of genomic DNA by using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above.

2.8.2 Results

1) Isolation of bacteria from the under surface of shoes

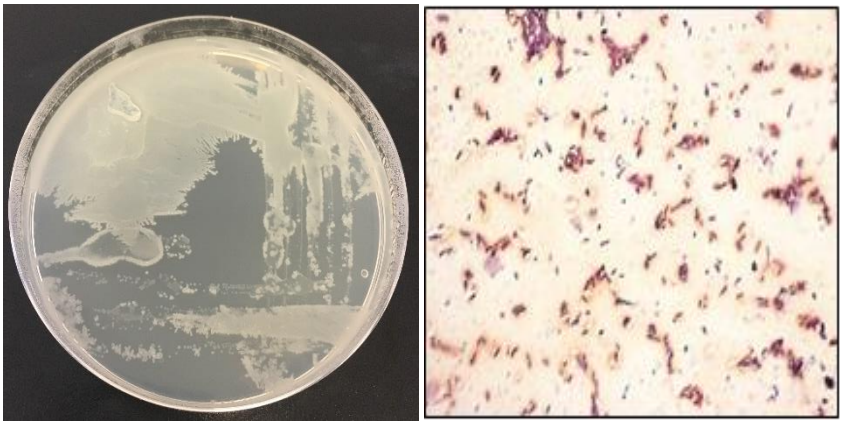
Bacteria were cultured using Nutrient Agar after isolation from the under surfaces of shoes.

2) Light microscope images. The isolates were examined under a light microscope (Figure 2.7) in order to establish that they were bacteria.



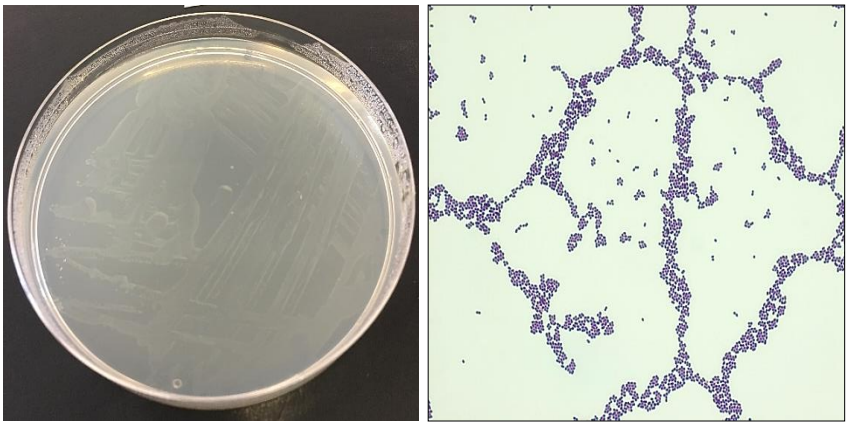
Escherichia coli LN558643.1

Gram stained. Magnification: 100x.



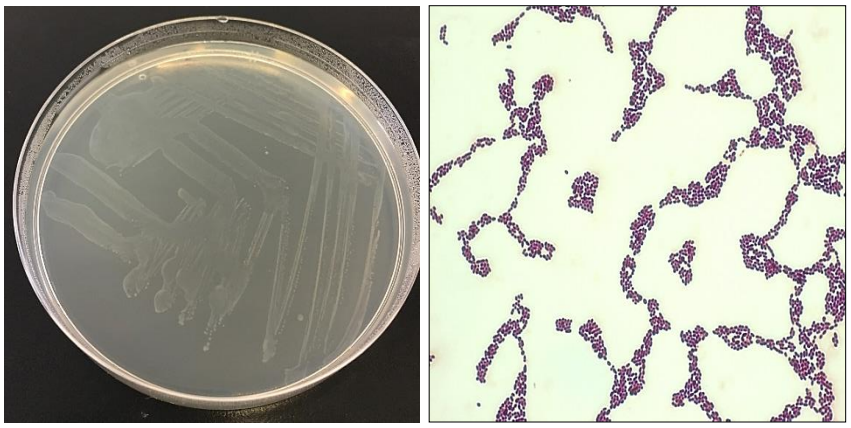
Bacillus licheniformis KP772335.1

Gram stained. Magnification: 100x.



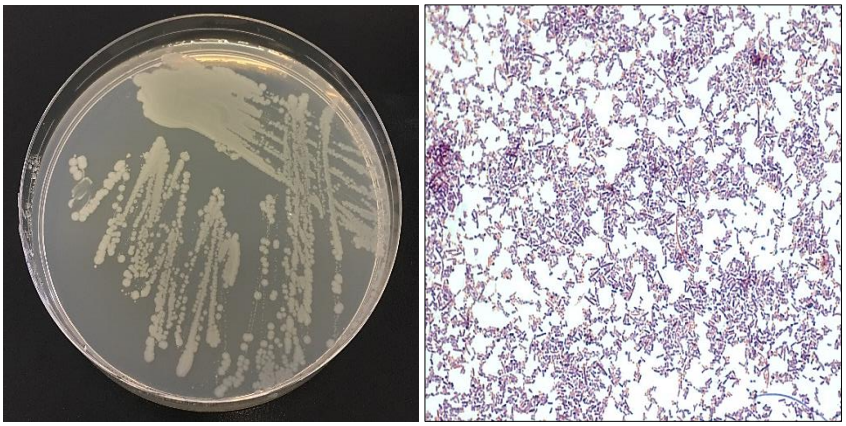
Enterococcus mundtii KR085796.1

Gram stained. Magnification: 100x.



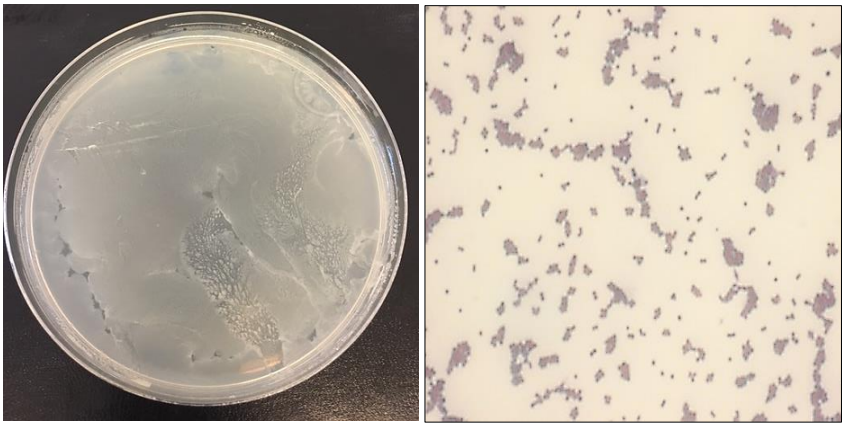
Enterococcus hirae KT261200.1

Gram stained. Magnification: 100x.



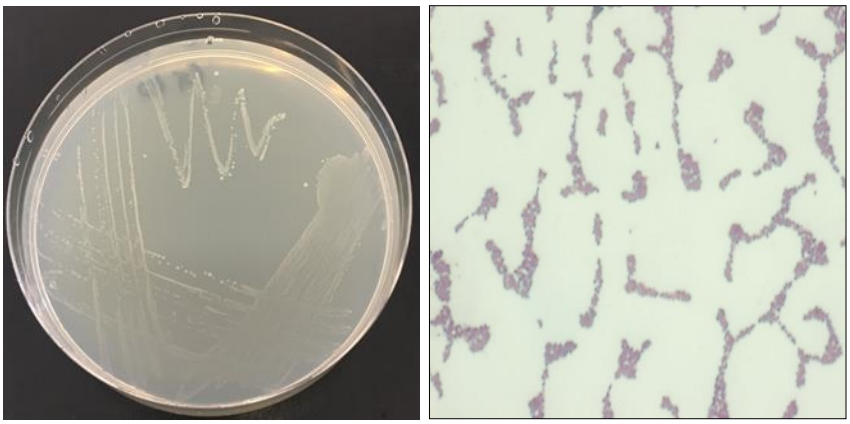
Bacillus licheniformis DQ071560.1

Gram stained. Magnification: 100x.



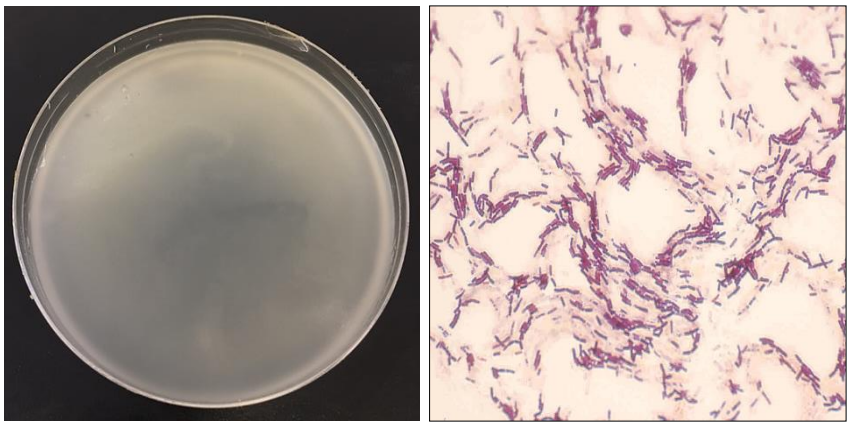
Brevibacillus borstelensis KT239000.1

Gram stained. Magnification: 100x.



Lysinibacillus fusiformis KP872952.1

Gram stained. Magnification: 100x.



Aneurinibacillus migulanus NR_113764.1

Gram stained. Magnification: 100x.

Bacillus subtilis EF488088.1

Gram stained. Magnification: 100x.

Figure 2.7: Nutrient Agar plates showing cultured bacteria isolated from the under surface of shoes, and also microscopy images showing the bacteria under the light microscope.

Table 2.8: Bacteria isolated from the under surfaces of shoes.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
G1	*Escherichia coli*	99%	LN558643.1
G2	*Brevibacillus borstelensis*	98%	KT239000.1
G3	*Bacillus licheniformis*	99%	KP772335.1
G6	*Enterococcus mundtii*	99%	KR085796.1
G7	*Enterococcus hirae*	98%	KT261200.1
G9	*Bacillus licheniformis*	99%	DQ071560.1
G10	*Lysinibacillus fusiformis*	99%	KP872952.1
G13	*Aneurinibacillus migulanus (Bacillus brevis)*	99%	NR_113764.1
G14	*Bacillus subtilis*	99%	EF488088.1

Aneurinibacillus migulanus (Bacillus brevis)

Aneurinibacillus migulanus (formerly *Bacillus brevis*) produces the antibiotic peptide gramicidin S. The cells are rod shaped, motile, and peritrichous, and ellipsoidal spores are formed in swollen sporangia (Berditsch *et al.*, 2007). Colonies are flat and smooth on nutrient agar. This organism is positive for catalase activity, development of an alkaline pH in Voges-Proskauer broth, and has the ability to reduce of nitrate to nitrite (Berditsch *et al.*, 2007; Takagi *et al.*, 1993). *Bacillus brevis* is a common environmental organism which is not associated with human disease.

Escherichia coli

Escherichia coli is a Gram-negative, facultative anaerobic, rod-shaped, coliform bacterium that is commonly found in the lower intestine of warm blooded organisms. Most *E. coli* strains are harmless, but some serotypes can cause serious food poisoning (Liu, 2011). *E. coli* are part of the normal flora of the gut, and can bring benefit to their hosts by producing vitamin K_2 and by preventing colonization of the intestine with pathogens. This bacterium is expelled into the environment within faecal matter. Faecal transfer is the main route through which pathogenic strains cause disease. Virulent strains can cause gastroenteritis, urinary tract infections, and neonatal meningitis. *E. coli* are a major cause of urinary tract infections (Liu, 2011).

Lysinibacillus fusiformis

The is a Gram-positive rod with motile spore arranged in 2-3 chains. It is frequently isolated from groundwater-derived drinking. Wenzler *et al*., (2015) report a case of severe sepsis caused by persistent *Lysinibacillus fusiformis* and *Paenibacillus* bacteraemia in a patient with a history of intravenous drug abuse and splenectomy; report a rare case of bacteraemia due to *Lysinibacillus* and *Paenibacillus spp.* in an immunocompetent patient without the involvement of implanted prosthesis or intravascular catheters (Rajesh *et al*., 2013; Ahmed *et al*., 2007; Wenzler *et al*., 2015).

Enterococcus mundtii

Members of the genus *Enterococcus* are Gram-positive ovoid cells that appear singly, in pairs, or in short chains and are catalase- and oxidase-negative; facultative anaerobes; and homofermentative, with lactic acid being the end product of glucose fermentation. Surface colonies on blood agar or nutrient agar are circular, smooth, and entire. Enterococcal infections are a major health concern, and as nosocomial pathogens, they often prolong hospital stays. *Enterococcus mundtii* can cause postoperative endophthalmitis, although it is rarely identified in endogenous endophthalmitis (Higashide *et al*., 2005).

Enterococcus hirae

Enterococcal disease comprises upper and lower airway, wound, hepatobiliary, intra-abdominal and urinary tract infections, meningitis, infective endocarditis and bacteraemia (including neonatal sepsis) (Poyart *et al.*, 2002). *E. hirae* has been reported to cause wound infections, gastritis, and occasional bacteraemia. It is a zoonotic pathogen rarely isolated from human infections. Poyart *et al*. (2002), however, found *E. hirae* colonized the native aortic-valve endocarditis in a 72-year-old man (Bourafa *et al.*, 2015; Poyart *et al*., 2002; Savini *et al.*, 2013).

The results show that a wide range of bacteria could be isolated from the soles of shoes worn in normal use. This reality is reflected by the fact that in critical care facilities, visitors and staff are made to wear flexible plastic overshoes to prevent microbial contamination from outside (Falvey and Streifel 2007; Lai, 2001; Mehta, 1990).

2.9 Isolation of bacteria from books and shelves in libraries and archive storerooms

Libraries and archives act as collections for the storage of large amounts of books and documents which are affected by a variety of different environmental factors including: microclimate in store rooms (i.e. temperature and humidity of the air), type and the amount of light (i.e. type of light waves on the electromagnetic

spectrum and radiation intensity), the type and amount of chemicals used for hygiene purposes and the air quality present in storage rooms. Books or other archival materials are a rich reservoir of many nutritional substances, such as cellulose, which is the main constituent of paper, and proteins, which are present in leather books. These nutritional substances stimulate the growth of a specific group of microorganisms (Kalwasińska *et al.,* 2012). Fungi are particularly strong cellulose decomposers, with species being represented, including members of *Botrytis, Chaetomium, Trichoderma, Penicillium*, while those fungi which exhibit strong proteolytic activity include species of the genera *Mucor, Aureobasidium, Chaetomium, Trichoderma, Verticillium and Epicoccum*. Bacteria however, are only infrequently found on paper, except where it is very damp when species of *Cellulomonas, Cellfalciculata, Cellvibrio* and *Cytophaga* tend to predominate (Kalwasińska *et al.*, 2012).

2.9.1 Materials and Methods

Sterile cotton swabs were wetted by dipping them in saline and used to collect samples from books and shelves in libraries and archive storerooms (Western Bank Library and the Information Commons, University of Sheffield). All samples were labelled and streaked on to nutrient agar plates; the plates were then incubated at 25°C under aerobic conditions for 24 hrs. After incubation the colonies were identified using 16S rRNA. Extraction of genomic DNA was by

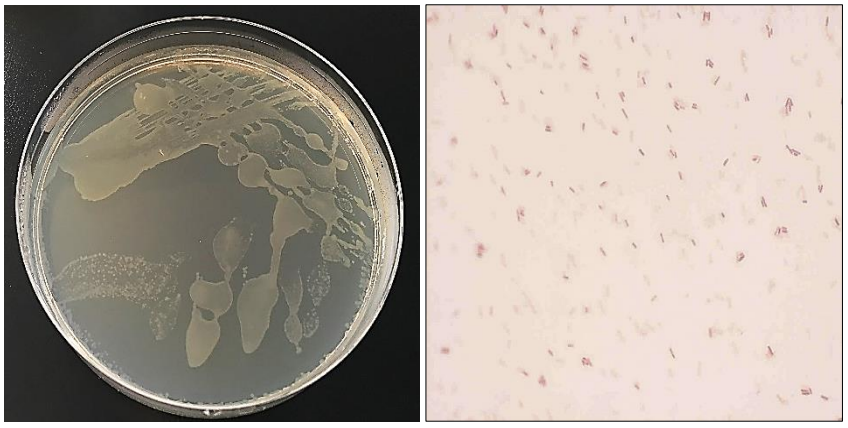
using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above**.**

2.9.2 Results

1) Isolation of bacteria from books and shelves in libraries and archive storerooms

Bacteria were cultured using Nutrient Agar after isolation from books and shelves.

2) Light microscope images. The isolates were examined under a light microscope (Figure 2.8).



Pseudomonas jessenii LN774645.1

Gram stained. Magnification: 100x.

Bacillus cereus KP192930.1

Gram stained. Magnification: 100x.

Bacillus altitudinis KT758615.1

Gram stained. Magnification: 100x.

Bacillus pumilus KP322017.1

Gram stained. Magnification: 100x.

Acinetobacter lofwii KT387352.1

Gram stained. Magnification: 100x.

Bacillus licheniformis DQ071560.1

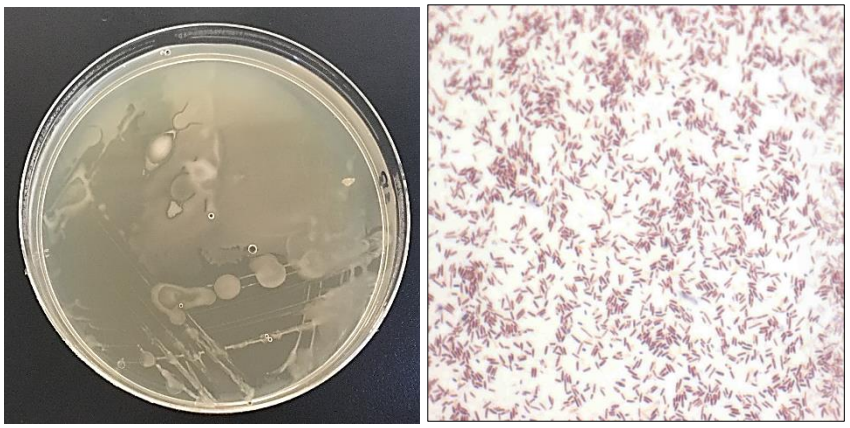
Gram stained. Magnification: 100x.

Bacillus megaterium KU550043.1

Gram stained. Magnification: 100x.

Staphylococcus succinus KJ888125.1

Gram stained. Magnification: 100x.

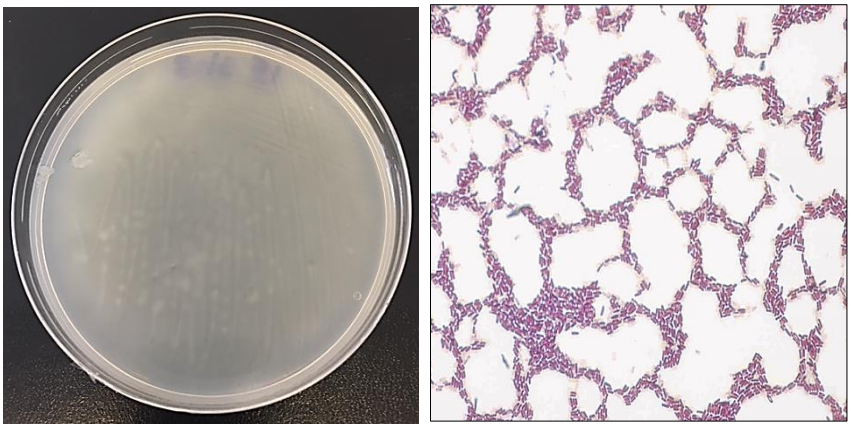


Bacillus stratosphericus KJ672335.1

Gram stained. Magnification: 100x.

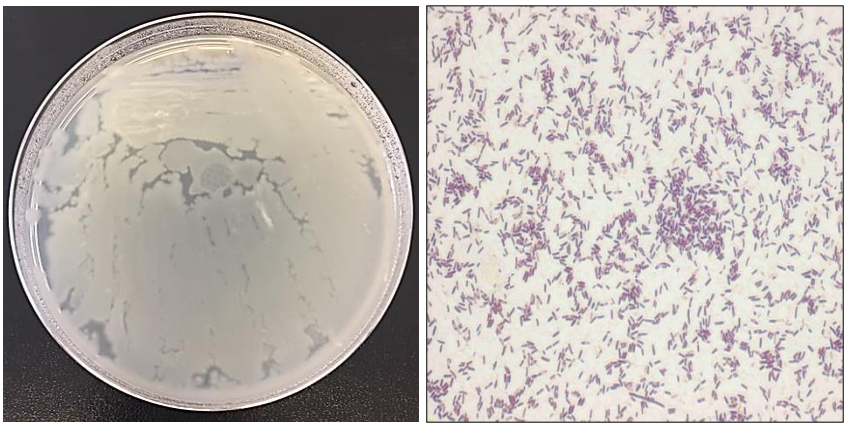
Bacillus licheniformis KT200463.1

Gram stained. Magnification: 100x.



Bacillus pumilus KU230023.1

Gram stained. Magnification: 100x.



Bacillus weihenstephanensis KC527665.1

Gram stained. Magnification: 100x.

Figure 2.8: Nutrient Agar plates showing cultured bacteria isolated from various from books and shelves in libraries and archive storerooms, and also microscopy images showing the bacteria under the light microscope.

Table 2.9: Bacteria present in dust settled on the surfaces of books and archive materials in the studied storerooms.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
9B3	*Pseudomonas jessenii*	99%	LN774645.1
3 SH11	*Bacillus cereus*	99%	KP192930.1
4 SH8	*Bacillus altitudinis*	98%	KT758615.1
7 SH11	*Bacillus pumilus*	98%	KP322017.1
1 SH6	*Bacillus stratosphericus*	98%	KJ672335.1
4 SH11	*Bacillus weithenstephanensis*	98%	KC527665.1
16 SH3	*Acinetobacter lofwii*	99%	KT387352.1
10B2	*Bacillus licheniformis*	99%	DQ071560.1
12SH4	*Bacillus megaterium*	99%	KU550043.1
14SH2	*Staphylococcus succinus*	99%	KJ888125.1
15SH3	*Bacillus pumilus*	99%	KU230023.1
2SH11	*Bacillus licheniformis*	99%	KT200463.1

Acinetobacter lwoffii

The genus *Acinetobacter* are Gram-negative, strictly aerobic, non-fermenting, non-fastidious, non-motile, catalase-positive, oxidase-negative, rod-shaped bacteria. *Acinetobacter* spp. are widely distributed in soil, water, vegetables, and are frequently isolated from animals and humans *Acinetobacter lwoffii* is part of the communal microflora on human skin and mucous membranes and causes nosocomial infections like septicaemia, pneumonia, meningitis, urinary tract infections, skin and wound infections (Regalado *et al.*, 2009) and is associated with polluted water systems (Liu, 2011).

Staphylococcus succinus

This is a Gram-positive, spherical bacterium which forms characteristic rosettes with one central cell surrounded by two to five peripheral cells; strains can be isolated from clinical specimens such as blood culture, pus, cerebrospinal fluid, exudate, eye and wound swabs (Liu, 2011).

Bacillus weihenstephanensis

Bacillus weihenstephanensis is a psychrotolerant species capable of growing at temperatures as low as 4°C–6°C is implicated in food spoilage and in foodborne illnesses (Liu, 2011).

Bacillus altitudinis

Colonies are Gram-positive, rod-shaped, endospore-forming and catalase-positive bacteria. Colonies on nutrient agar are white, convex with a regular margin and 2–3 mm in diameter (Shivaji *et al.,* 2006). Growth occurs between 8˚C and 45˚C and at pH 5–8. *B. altitudinis* was isolated from cryogenic tubes used for collecting stratospheric air samples from high altitudes (Shivaji *et al*., 2006). Its pathogenicity is unknown.

Bacillus pumilus

Bacillus pumilus is one of many species within the genus *Bacillus* which have emerged as novel foodborne human pathogens that cause severe fatal infections (Kimouli *et al.,* 2011). This bacterium has also been reported to cause infectious endophthalmitis and a case of central venous catheter infection with *Bacillus pumilus* in immunocompetent patients. *Bacillus pumilus* is a member of the intestinal flora of humans and can produce exotoxins that are cytotoxic for cultured mammalian cells (Kimouli *et al.,* 2011).

Bacillus stratosphericus

Colonies on nutrient agar are white, irregular, and raised. Growth occurs between 8˚C and 37˚C, but not at 40˚C (Shivaji *et al.*, 2006). *Bacillus stratosphericus* were isolated from cryogenic tubes used to collect air samples at altitudes of 24, 28 and

41km. Also it was isolated from cryogenic tubes used for collecting air samples from high altitudes (Shivaji *et al.*, 2006). Its pathogenicity is unknown.

Bacillus megaterium

Bacillus megaterium is a Gram-positive, mainly aerobic spore-forming bacterium found in soil, seawater, sediments, rice paddies, honey, fish, and dried food. It is not regarded as an important human pathogen (Scholle *et al.*, 2003)

Pseudomonas jessenii

Cells are Gram-negative, asporogeneous and rod shaped motile by means of single polar flagellum. Colonies are smooth on nutrient agar circular non-pigmented and non-haemolytic when they are grown on blood agar. It is not regarded as human pathogen (Verhille *et al.*, 1999).

2.9.3 Discussion

The most frequently isolated bacteria belong to the genus *Bacillus* which is a Gram-positive rod (Table 2.9), while Gram-positive cocci were represented by *Staphylococcus* spp. Gram-negative rods, like *Pseudomonas jessenii* were also isolated, as was *Acinetobacter lofwii*, a non-fermentative Gram-negative a member of the genus *Acinetobacter*. Most of the identified microorganisms have been

previously isolated from a wide variety of different materials such as leather, paintings and books (Karbowska-Berent *et al.*, 2011). *Bacillus* may cause the decomposition of adhesives in paper and book bindings. *Bacillus* has the ability to transform into spores allows them to preserve viability in unfavourable, dry conditions for a long period of time. Owing to that, these bacteria were the most numerous species in settled dust (Karbowska-Berent *et al.*, 2011).

2.10 Isolation of bacteria from the upper surface of water taps

Hospital water systems often act as a source of nosocomial infection, particularly among immunocompromised and high-dependency patients (notably in intensive care units) (Boyles *et al.*, 2012). Patients are exposed to waterborne microorganisms in hospitals when bathing, showering or washing hands following direct contact with contaminated fixtures (e.g. wash-basins and taps); by ingestion of water; via indirect contact (e.g. medical equipment rinsed with water); and by staff-transfer via medical equipment rinsed with water; and finally, by inhalation of aerosols produced by a water source, and the aspiration of contaminated water. Such microbes often originate from biofilms and sediments in supply water, water storage tanks, and water distribution network pipes as well as associated equipment (Boyles *et al.*, 2012). Water quality can become corrupted rapidly due to the formation of biofilms by bacteria in the supply water. Taps are frequently contaminated with biofilm-containing opportunistic pathogens, notably *P.*

aeruginosa, and numerous cases of cross-infection from hospital taps have been reported (Boyles *et al.,* 2012). Immunocompromised patients are particularly susceptible to infection by such microorganisms, which can cause bacteraemia, pneumopathy, meningitis, and other conditions. *Pseudomonas aeruginosa* is particularly often isolated from these sources and has been reported to be lethal in 50%, 70%, and 20% of bacteraemia, pneumopathy, and meningitis cases, respectively (Boyles *et al.,* 2012).

2.10.1 Materials and Methods

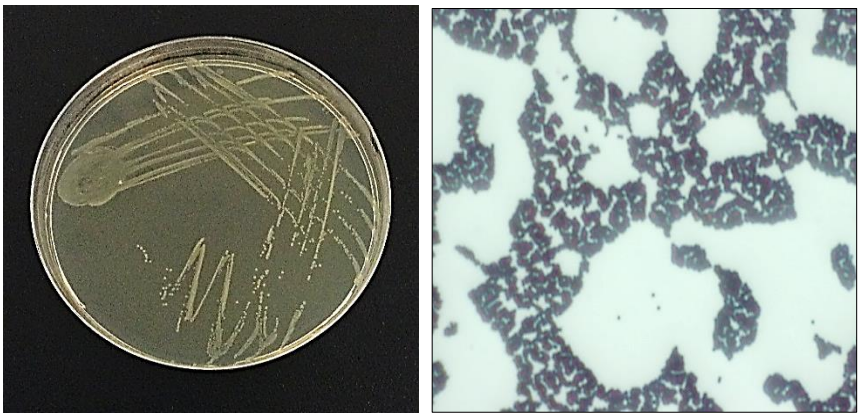
Sterile cotton swabs were wetted by dipping them in saline and used to collect samples from tops of water taps in toilets in Firth Court and the Student Union Building (University of Sheffield), and from volunteer house owners. All samples were labelled and streaked on to Nutrient Agar plates; the plates were then incubated at 25°C under aerobic conditions for 24 hrs. After incubation, the colonies were identified. Genomic DNA extracted from each isolate was identified using 16S rRNA. The extraction of genomic DNA was by using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. The methods used for preparation of PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis are detailed above.

2.10.2 Results

1) Isolation of bacteria from the upper surface of water taps

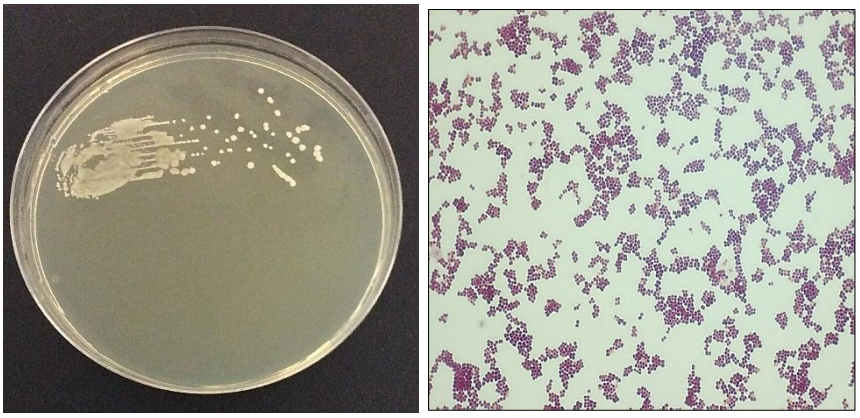
Bacteria were cultured using Nutrient Agar after isolation from the upper surface of water taps.

2) Light microscope images. The isolates were examined under a light microscope (Figure 2.9).



Delftia lacustris KT958881.1

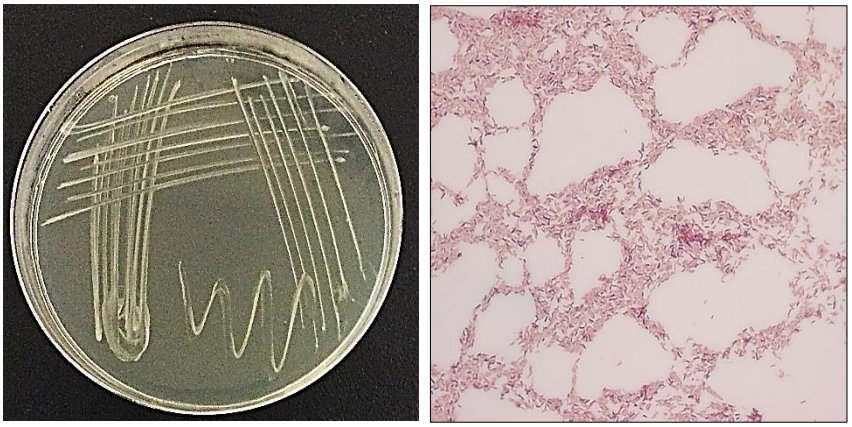
Gram stained. Magnification: 100x.



Rothia amarae NR_029045.1

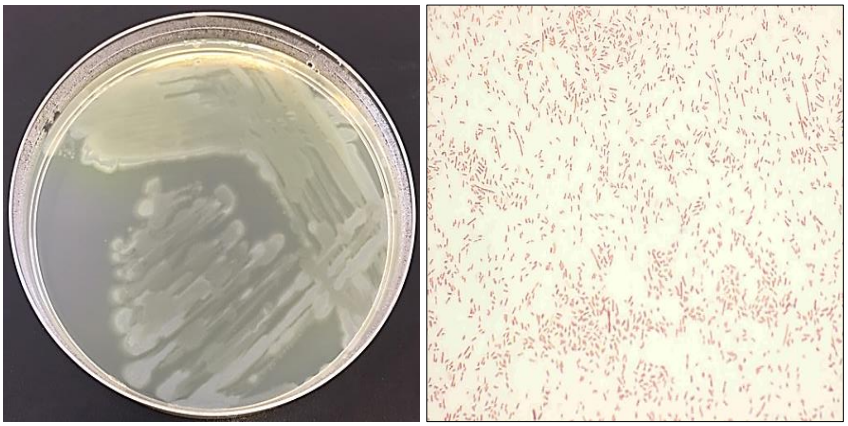
Gram stained. Magnification: 100x.

Delftia acidovorans (comamonas acid) JX090199.1. Gram stained. Magnification: 100x.



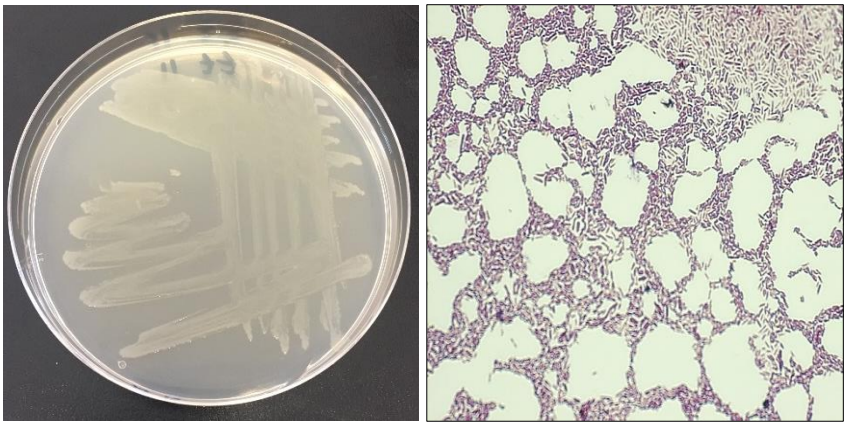
Arthrobacter sanguinis NR_044399.1

Gram stained. Magnification: 100x.



Pseudomonas aeruginosa KF680991.1

Gram stained. Magnification: 100x.



Bacillus cereus GQ344804.1

Gram stained. Magnification: 100x.

Figure 2.9: Nutrient Agar plates showing cultured bacteria isolated from the top-surface of water taps, and also microscopy images showing the bacteria under the light microscope.

Table 2.10: Bacteria isolated from the upper surface of water taps.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
2tt	*Staphylococcus epidermidis*	98%	KT887972.1
3tt	*Rothia amarae*	99%	NR_029045.1
4tt	*Acinetobacter johnsonii*	99%	KP763485.1
6tt	*Delftia lacustris*	99%	KT958881.1
7tt	*Pseudomonas aeruginosa*	98%	KF680991.1
8tt	*Delftia acidovorans (comamonas acid)*	99%	JX090199.1
9tt	*Arthrobacter sanguinis*	99%	NR_044399.1
10tt	*Delftia acidovorans (comamonas acid)*	98%	KJ781879.1
11tt	*Bacillus cereus*	94%	GQ344804.1

Pseudomonas aeruginosa

Pseudomonas spp. act as opportunistic pathogens with *P. aeruginosa* being the most clinically significant as a major cause of lower respiratory tract, bloodstream, and urinary tract infections, particularly among patients in intensive care units or with compromised immunity (Liu, 2011). This bacterium is often isolated from

moist environments within health care settings, such as taps, toilets, showers, respiratory equipment, and cleaning solutions. *Psuedomonas aeruginosa* is a major pathogen in chronic lung diseases, most notably in cystic fibrosis. It causes infections in critically ill patients in intensive care units, burn patients, and particularly when immunocompromised (Liu, 2011). Such infections include ventilator-associated pneumonia, catheter-related bloodstream or urinary tract infections; other infections are derived from medical devices or penetrating trauma, sepsis in neutropenic cancer and transplant patients, skin and soft-tissue infections in burn and diabetic patients, postoperative endophthalmitis and necrotizing otitis externa in diabetics (Liu, 2011).

Delftia acidovorans (Comamonas acidoverans)

Cells of this bacterium are Gram-negative straight to slightly curved rods, which occur singly or in pairs. They are motile and are oxidase and catalase positive. This organism has been isolated from serious infections such as central venous catheter-associated bacteraemia, corneal ulcers, otitis media exist (Khan *et al.*, 2012). *Delftia acidovorans* infections have also been reported from cases of endocarditis, ocular infections, acute suppurative otitis media, bacteraemia, urinary tract infections, intravascular catheter related infections and empyema; serious infections have been found amongst immunocompromised patients. Patients with indwelling devices are at particular high risk of acquiring *Delftia acidovorans* infections (Khan *et al.*, 2012).

Acinetobacter johnsonii

Acinetobacter spp. have been isolated from a variety of opportunistic infections, including septicaemia, pneumonia, endocarditis, meningitis, skin and wound infection, and urinary tract infection. *Acinetobacter spp*. (e.g., *A. johnsonii*) have been shown to form an important component of the communal microflora on human skin and mucous membranes (Bergogne-Bérézin *et al*., 1996)

Rothia amarae

All *Rothia* species are Gram-positive and are isolated from humans or animals as well as from soil and water. They are particularly associated with dental caries and periodontal disease notably in immunocompromised hosts, but rarely in healthy hosts. Clinical syndromes linked to *Rothia* infection include bacteraemia, endocarditis, meningitis, peritonitis, bone and joint infections, pneumonia, skin and soft tissue infection, endophthalmitis, and prosthetic device infection (Fan *et al*., 2002; Xion *et al*., 2013; Ramanan *et al*., 2014).

Arthrobacter sanguinis

Arthrobacter are Gram-positive aerobic bacilli commonly found in the environment, although they can also cause endophthalmitis after intra-ocular implantation, infective endocardites in intravenous drug- abuser, featal demise and disseminated intravascular coagulation in pregnant women and catheter-related bacteraemia in leukemic patients (Mages *et al.*, 2008; Yap *et al.*, 2015). *Arthrobacter* infections are often difficult to diagnose using conventional

biochemical assays. *Arthrobacter* related peritonitis can be successfully treated with appropriate parenteral antibiotics without the need for catheter removal (Mages *et al*., 2008, Yap *et al*., 2015).

2.11 Determination of the number of bacteria on hands after washing and drying normally and with warm air hand dryer

2.11.1 Introduction

Hand drying represents the final part of the hygiene procedure in a public toilets and if the toilet is designed well, the number of surfaces which the user subsequently touches will be limited or reduced to near zero. This is essential because wet hands can spread up to one thousand times more bacteria than can dry hands (Smith, 2009). This is essentially because water transfers easily between surfaces and because bacteria do best in moist environments (Redway and Fawdar, 2008). As a result, it is critical that hands are not contaminated with bacteria due to the drying process (Harrison *et al*., 2003). The most frequently used means of hand drying are paper towels, hot air dryers, jet air dryers and cloth towels. It has been suggested that air dryers should be avoided as they accumulate aerosols from toilets which then contaminate hands (Snyder, 1998). This last mentioned author concludes that the use of paper towels decreases the number of bacteria on hands, while hot-air dryers conversely increased contamination by some bacteria; a finding suggestion that has been widely debated (Holah, 2011); many contend

however, that hot air dryers are often slow and inefficient, leaving the hands of users moist and possibly still contaminated. Cloth roller towels are similarly not recommended essentially because they are generally of low capacity, and when a roll comes to an end it becomes available for common use and is therefore likely to increase the spread of pathogens (Snyder, 1998).

This work was undertaken with the aim of evaluating the performance of warm air hand driers, in toilets relative to bacterial contamination. First, the ability of warm air driers to dry hands hygienically was evaluated by measuring the number of microorganisms on different working days. Secondly, it was determined if warm air driers influence the level of air-borne microorganisms in the washroom environment, as was suggested by Knights *et al.* (1993). Finally, the surfaces of warm air driers and other washroom areas were examined for total viable counts in order to determine if the use of air driers affects bacterial distribution.

2.11.2 Materials and Methods

General purpose, non-antimicrobial bar soap was used for hand washing. Hands were wetted with tap water, and the soap applied and lathered together vigorously for 5 minutes, covering all surfaces of hands followed by rinsing with tap water. Finally, the hands were shaken five times in order to remove of excess water before drying. Areas of the washed hands were applied to the surface of Nutrient Agar plate; the plates were then incubated at 37°C for 48h. Warm air hand-dryers were next used for hand drying; the air temperature applied was 0°C -40°C at a

distance of 15 cm. When hands were placed in the 15 cm drying space, warm air flowing automatically was turned on. During drying, hands were either rubbed or had their palms turned upward and were held stationary. Then dried hands and fingers top were touched onto the surface of nutrient agar plate. The plates were incubated at 37°C for 48 h and scored for the presence or absence of growing bacteria.

2.11.3 Results

The results show that no bacteria were isolated from hands dried in the normal way, but were isolated from hands when dried using an air dryer.

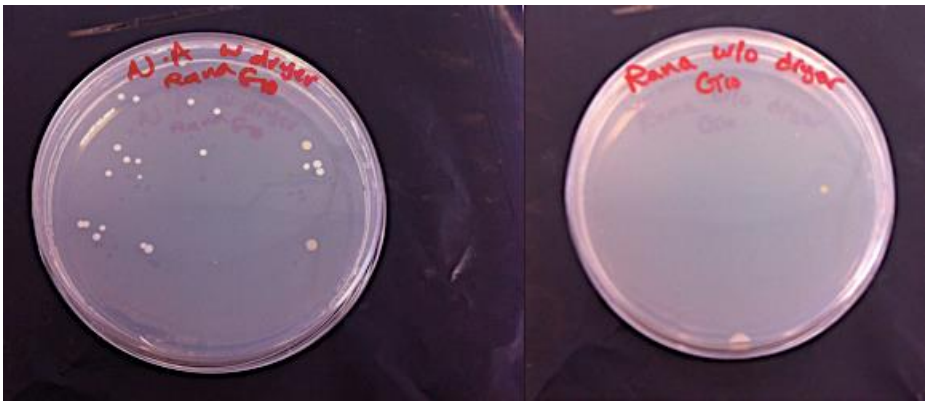


Figure 2.10: Agar plates used to for the assessment of bacterial contamination on hands. (Left) hand washed and dried with a warm air hand dryer, (Right) hand washed and dried without warm air dryer.

2.12. Quantification of bacteria transferred from hand warm air dryers

2.12.1 Materials and methods

Nutrient Agar plates were used in this experiment to isolate the transferred bacteria from hand warm air dryers. Any bacteria transferred to the plates from the hot air driers were counted and the effect of drying times was determined.

2.12.2 Results

Table 2.11: Showing the mean of the bacteria count using three different types warm air dryer (WAD,1-3) for different drying times.

	5 Sec	10 Sec	15 Sec	20 Sec	25 Sec	30 Sec	35 Sec	40 Sec	45 Sec	50 Sec	55 Sec	60 Sec
WAD1	0	2	5	6	3	9	12	10	23	41	31	30
WAD2	12	17	18	22	18	16	50	37	15	49	44	63
WAD3	19	20	15	24	10	8	11	20	18	19	21	30

Table shows that there was a correlation between the drying time and the resultant bacterial counts, with the counts generally increasing with the drying time exceeding 30 seconds. Redway and Fawdar (2008) investigated the spread of

contamination from different drying methods and concluded that microorganisms were spread significantly further when an air blade dryer was used instead of paper towels. While not significant if only non-pathogenic microorganisms are spread, the risk of pathogen contamination of the environment will result when pathogens are present on hands and are liberated into the air (Blackmore, 1989).

2.12.3 Discussion

From the results presented in this Thesis, it is clear that hand dryers distribute bacteria into the surrounding air. As has been mentioned elsewhere in this Thesis, many of these bacteria, even when not direct pathogens, pose a potential problem for immunocompromised patients here. Hand dryers have recently become increasingly popular and for reasons of cost, these machines are often supplied in place of traditional cloth and paper towels (Huang *et al*., 2012). This does not present a health problem for most hospital patients and visitors (except where immunocompromised). The use of hand dryers in medical settings should therefore be reviewed and, if necessary, they should be replacing by traditional approaches, the consensus being that paper towels are the preferred method of hand drying in such settings (Best *et al.*, 2014; Huang *et al.*, 2012).

2.13. General Discussion regarding potential pathogens in the environment

Boyce *et al.,* (1997) have shown that surfaces in hospitals are often contaminated with MRSA, as are staff. This points out the necessity of using detergents and antibacterial wipes to reduce bacterial loads, especially postoperative MRSA. Vancomycin-resistant enterococci (VRE) can achieve long-term survival in medical environment, even following extensive cleaning and disinfection. Pathogens can, in fact, often be spread when cleaning cloths are a) re-used on surfaces, b) when little contact time between a surface and the applied disinfectant, and c) when surface are casually sprayed and wiped instead of being aggressively scrubbed. VRE appears to be particularly efficient at surviving successive disinfection, regimes, even so-called "double bleach-based cleaning".

Disinfectants can be effective if hospital surfaces are scrubbed daily and when this is associated with a hand cleaning programme. The surface screening of cultures has also proved effective, as has the use of 5% sodium hypochlorite to clean all surfaces at least three times daily. Both MRSA and VRE can survive for long periods which presents an obvious risk in relation to the movement of patients into rooms which have been previously occupied by infected patients.

Hospital sinks are an obvious source of pathogenic bacteria, with antibiotic resistant *Klebsiella pneumoniae* strains showing particularly extended survival within plumbing thereby, in extreme cases, necessitating the replacement of sinks and related pipe-work. Pathogen survival is also linked to biofilms adhering to

surfaces on sinks and associated plumbing and unfortunately the use of chlorine-containing products is often ineffective and even prolonged use fails to destroy all biofilms thereby necessitating the physical disruption of any biofilm which is found to be growing in contaminated plumbing systems.

2.13.1 Antimicrobial surfaces

Some high-tech solutions are currently available to control surface pathogen contamination, by so-called, "self-sanitizing surfaces" which include hard metals (e.g. copper and silver) and novel materials such as light-activated titanium dioxide-containing surfaces which prevent the accumulation of surface microbes (Dancer, 2014). Several types of antimicrobial surfaces including antiadhesive coatings, and antimicrobial coatings exist including **Triclosan (**Microban triclosan): which is used on surfaces and in many antibacterial liquid and bar soaps and 30% of bar soaps, although evidence for resistance is developing. **Silver: S**ilver ions (Ag^+) bind to thiol (−SH) groups in microbial enzymes and proteins and lead to microbial-cell inactivation; such coatings are not, however, permanently active and resistance can develop (Dancer, 2014). **Copper:** Copper (as will be discussed below) is also toxic to pathogens and coatings can be used to reduce microbial contamination. **Polycationic antimicrobial surfaces:** these are surfaces which are treated with hydrophobic, negatively charged poly-cations which kill bacteria by bringing about physical damage to the cell-envelope. **Light-activated antimicrobial surfaces:** These produce unselective, reactive radicals

which kill a range of microorganism and reduce the chances of resistance developing. Two types are available, the first is based on a photosensitizer immobilized within a coating, while the second is a coating which contains a titanium dioxide (TiO_2)-based catalyst (Dancer, 2014).

CHAPTER 3

STUDIES ON SURVIVAL OF BACTERIA ON VARIOUS SURFACES

3.1 Studies on the survival of bacteria on smooth and rough unglazed ceramic tiles under ambient conditions

3.1.1 Introduction

Ceramic tiles are frequently used in the built environment, notably in hospitals and provide an obvious survival environment for potentially pathogenic microorganisms. Ceramic tiles are widely used in domestic and health care settings. They are obviously advantageous in being durable, water repellent, easy to keep clean, and are readily exposed to bacteria-killing sunlight. The grouting between tiles may however, act as a reservoir for microbes, including pathogens. Tile surfaces differ, between smooth and rough. Logically, one would assume that rough, unglazed tiles would provide a more suitable environment for microbes and as a result, these are generally preferred for use in health-care settings. The aim of this work was to determine the survival (in the ambient environment) of a variety of bacteria on smooth (glazed) and rough (unglazed) tiles.

3.1.2 Materials and Methods

Ceramic tiles having either smooth or rough surfaces (9 cm^2) were firstly sterilized by autoclaving (Figure3.1). The test bacteria were then grown on Nutrient Agar medium as a pure culture, while yeasts (*Candida albicans* and *C. rugosa* were

grown on Sabouraud Dextrose agar). Bacterial and yeast suspensions from colonies were prepared in sterile saline equal to McFarland 0.5 turbidity (the density of a bacterial suspension equal 1.5x 10^8 colony forming units CFU/ml). The tiles were inoculated by placing on their uppermost chosen surface approximately 10 microliters of either a bacterial or yeast suspension, which was allowed to outspread and dry under sterile conditions and left at room temperature (18-23°C). The tiles were transferred to sterile Falcon tubes containing sterile water and serial dilution counts were made.

In the second series of experiments, the tiles were inoculated with *Candia rugosa* and at the end of the same exposure period were washed and serial dilution plated onto Sabouraud Dextrose agar.

Figure 3.1: The two types of ceramic tiles used: A) smooth ceramic tile, B) rough ceramic tile.

3.1.3. Results

3.1.3.1 Bacterial survival on ceramic tiles

Figure (3.2) shows the number of *S. aureus* and *E. coli* bacteria isolated from the two tile types. Numbers of *S. aureus* on the rough tiles increased over the incubation period, while number on the smooth tiles decreased. In both cases however, bacteria were still present after 65h. In the case of *E. coli*, the number decreased over the incubation period, while there was a slight increase in the numbers of bacteria on smooth tiles (Figure 3.3). The results show that both *S. aureus* and *E. coli* can survive on both tile types over a 65 h period, a finding which is obviously relevant to pathogen survival and transfer in healthcare settings. Staphylococci are among the most resistant non-spore forming bacteria, and they can survive at various environmental conditions. They can be cultured from dried clinical material after several months. Yazgi *et al.* (2009) found that *S. aureus* survived on laminate for 75.4 days and inox sheet for 68.2 days, whereas these survival days were 73.8 days on ceramic tiles and 63.4 days on vinyl flooring. The length of survival of these organisms on the various materials may have significance for infection control in hospitals. For example, the ceramic tiles tested in this study are the material used for floors and walls of hospitals that are handled by both patients and staff when they are touched or cleaned. *Staphylococci* and *E. coli* survived for days on this covering materials, suggesting that they could act as reservoirs for such pathogenic bacteria.

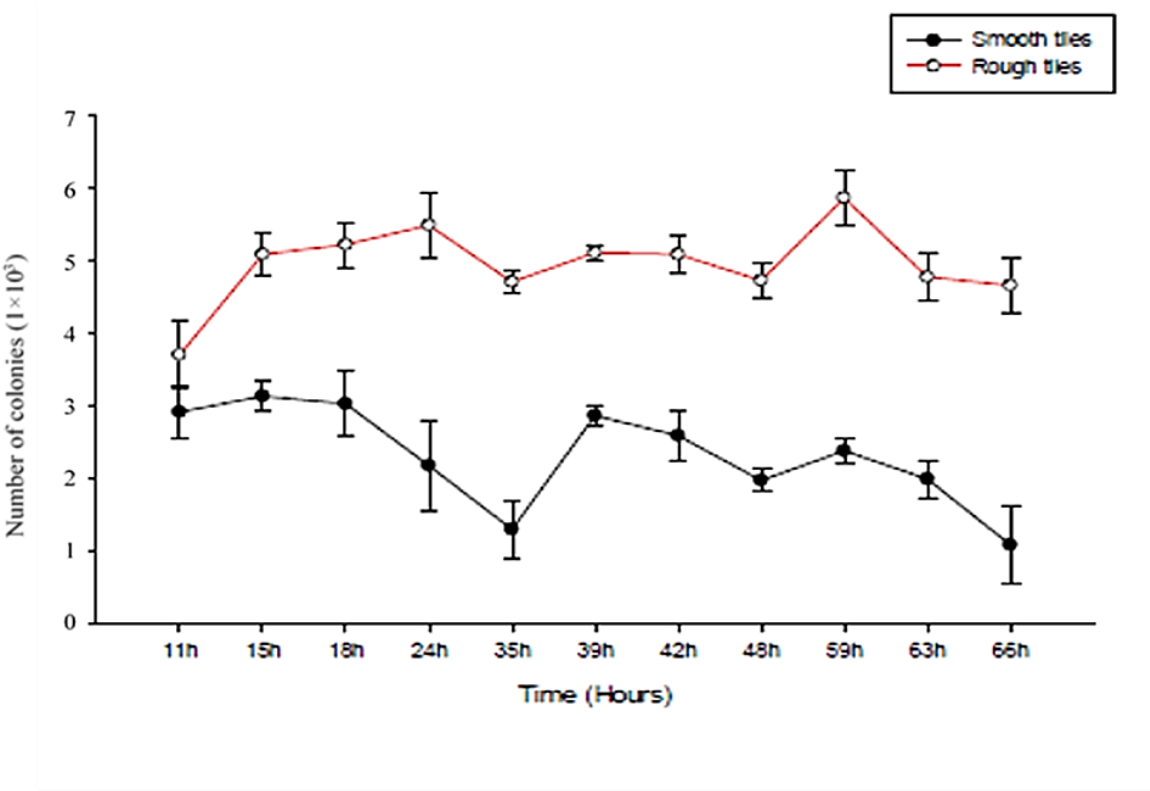


Figure 3.2: Survival of *S. aureus* on ceramic tiles during 65h.

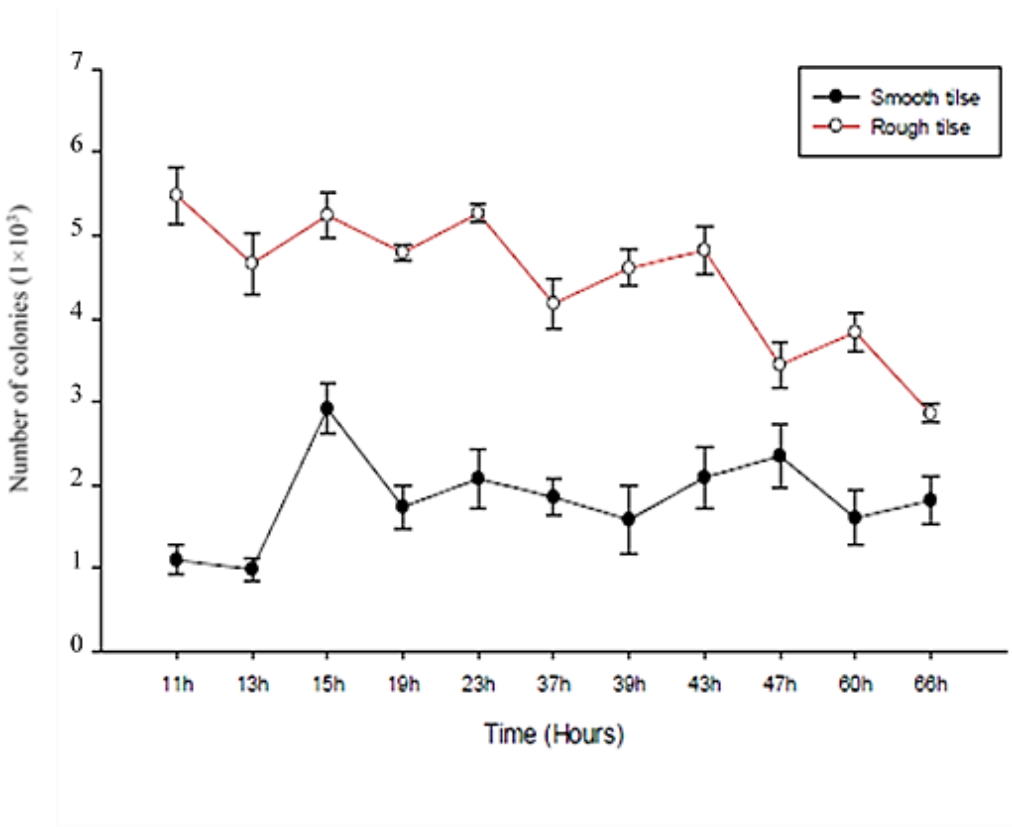


Figure 3.3: Survival of *E. coli* on ceramic tiles during 65h.

3.1.3.2 Yeast survival on ceramic tiles

The results (Figure 3.4) show that *Candida rugosa* survived for a period of 72h on both smooth and rough tiles with numbers generally increasing for 53-56h when they declined rapidly but the yeast was still present in a viable state after 72h.The yeast is associated with nosocomial infections in patients. Where comparisons are possible for the yeast data, this result agrees with Traoré *et al.* (2002) who found *C. albicans* and *C. parapsilosis* remained viable for at least 3 and 14 days when dried on surfaces materials.The results of the ability of *C. albicans* and *C. parapsilosis* to survive on glass and metal carriers over a 14-day period are summarized in a study by Traoré *et al.* (2002). *Candida parapsilosis* was found to survive much better than *C. albicans* on both types of non-porous surface. Also, *C. albicans* was undetectable at the end of the third day, while *C. parapsilosis* remained detectable even after 14 days under ambient conditions. There was a significant difference between the survival of *C. parapsilosis* and *C. albicans* after 14 days on glass carriers and stainless steel carriers. These results indicate that ceramic tiles play a role as reservoirs or vectors for fungi because those tested generally remained viable on these surfaces for many days. In this age of increasing antifungal resistance, these survival data indicate that the appropriate disinfection of the environment and control procedures should be used to control infections in hospitals.

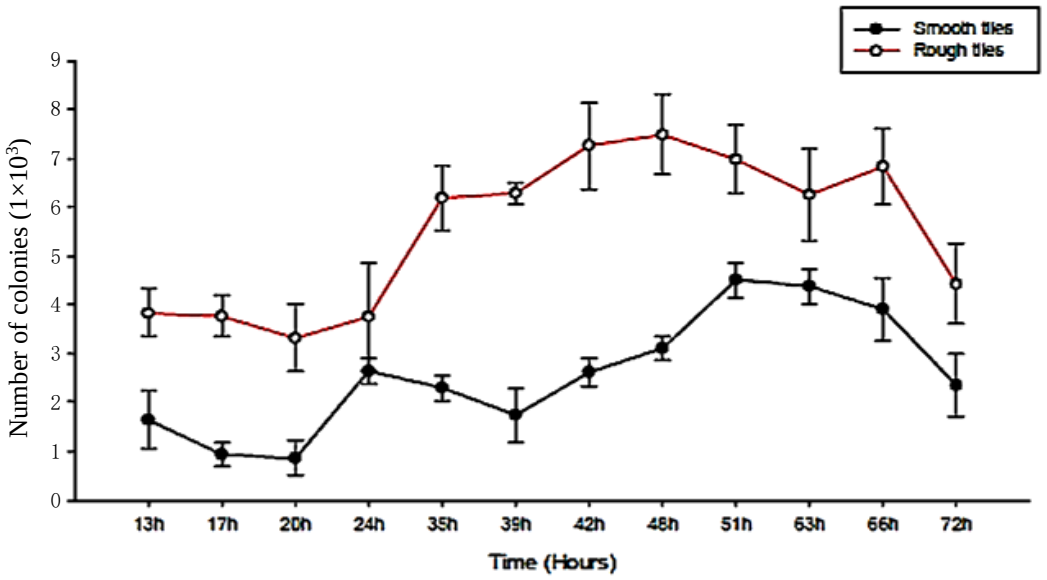


Figure 3.4: Survival of *Candida rugosa* on ceramic tiles.

3.1.3.4 Discussion

The most important factor in transmission of microorganisms in the environment is the ability of microorganisms to survive on environmental surfaces. The contamination and colonization of surfaces is important in relation to the transmission of nosocomial infections pathogens, such as methicillin-resistant *S. aureus* and vancomycin resistant Enterococci (VRE). For example, a range of floor covering materials are used in intensive care units, operating rooms, clinics, and laboratories of hospitals due to which influence the rate of microbial survival and as a result, need to be carefully chosen in order to minimize microbial colonization and survival. The preferred materials are smooth-surfaced and include ceramic tiles, laminates, inox sheets, and vinyl which are easy to disinfect

during cleaning. Neely and Maley (2000) studied the survival of several clinical and environmental *staphylococci* and *enterococci* on fabrics and plastic that are used in hospitals. They found that the survival period of *S. aureus* was more than 90 days on various surfaces, whereas it was 18 to more than 80 days for *enterococci*. It is clear from the results for both tiles and the study discussed in this Thesis that covering materials have a significant influence on the survival periods of bacteria. The Thesis results show that ceramic tiles play a role as reservoirs or vectors for the yeast, *C. rugose*, because this organism generally remained viable on these surfaces for many days. Strategies to reduce the rates of nosocomial infection with these pathogens should conform to established guidelines, with an emphasis on thorough environmental cleaning and use of Environmental Protection Agency–approved detergent-disinfectants.

3.1.4 Discussion

Bacterial and yeast survival was tested on both smooth and rough ceramic tiles. The results show that ceramic tiles provide reservoirs for microbes because the tested species generally remained viable on these surfaces for a number of days; the length of survival on both smooth and rough ceramic tiles being related to both the genus and the species. Clearly cleaning strategies aimed at maintaining low pathogen populations on hospital tiles, whether rough or smooth need to take such apparently anomalous findings into consideration.

3.2. Studies on the survival of bacteria on toothbrushes under ambient conditions

3.2.1 Introduction

The environment of the toothbrush is affected by many conditions whether it is the architecture of the toothbrush itself regarding bristles or by adjusting the pH level. These conditions alter the population of bacteria on the toothbrush. While the toothbrush is not the ideal niche for a microbe, the toothbrush is capable of supporting microbial life (Downes *et al.,* 2008).

3.2.2 Materials and methods

3.2.2.1 Bacterial survival on toothbrushes during a month

The new toothbrushes were prepared and were sterilized by 10% ethanol spray. The strains of the test bacteria were grown on the Nutrient Agar medium as a pure culture. Bacterial suspensions from the colonies were prepared in sterile saline equal to McFarland 0.5 turbidity. The toothbrushes were contaminated by placing on them on approximately 10 microliter volume of the bacterial suspension, and the inoculum allowed to outspread and dry itself under sterile conditions. Then the toothbrushes were kept at room temperature (18-23°C) (Figure 3.5). Beginning from the third day, toothbrushes were taken and placed in a sterile Falcon tubes contained sterile water. The numbers of viable organisms in the resultant suspension were determined by serial dilution and plating on to Nutrient Agar. The

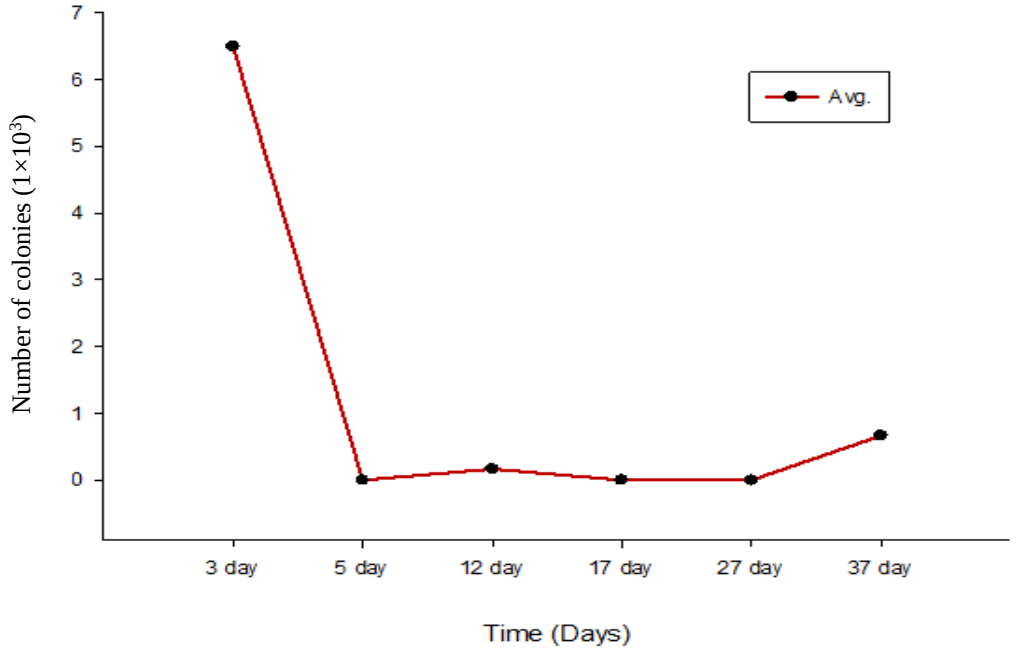
step was repeated after 5, 15, and 20 days and then the plates were incubated at 37°C for 48 h.

Figure 3.5: New toothbrushes inoculated with the bacterial suspension of *S. aureus* and *E. coli.*

3.2.3. Results and discussion

Numbers of inoculated *S. aureus* and *E. coli* on toothbrushes decreased after 5 days of storage (Figure 3.6 A, B) and then numbers remained constant (except for small increase in numbers of *S. aureus* at 37 days. *Escherichia coli* also survived for 5 days on tested toothbrushes.

A)



B)

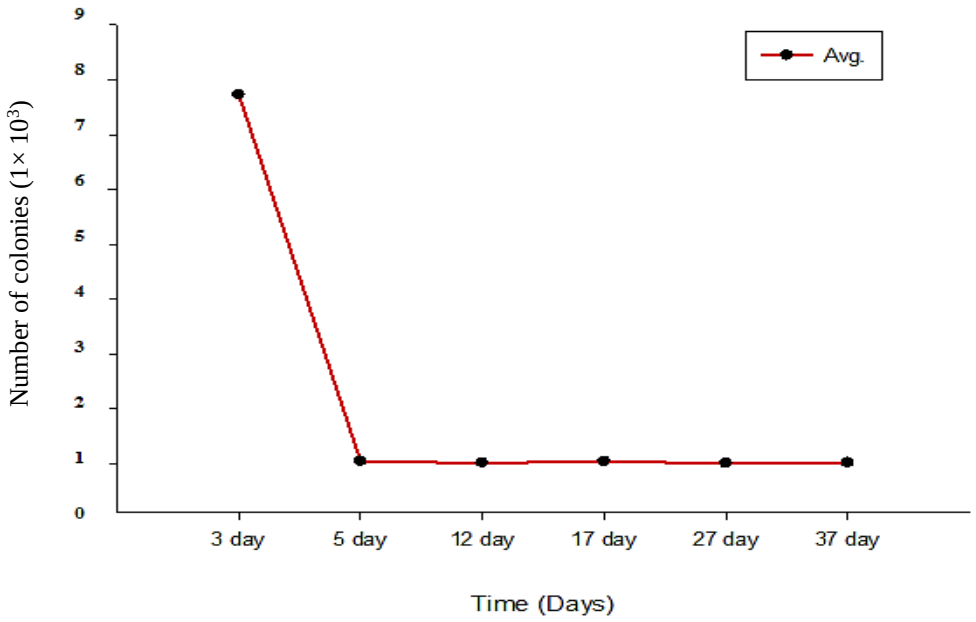


Figure 3.6: Population density of *Staphyolcoccus aureus* (A) and *E. coli* (B) when inoculated onto toothbrushes (analysis of variance).

* All values after 5 days were significantly different from control (p=0.05)

3.2.4 Discussion

The aim of this study was to compare bacterial survival on new conventional toothbrushes in the laboratory. The survival times of *Staphylococcus aureus* and *E. coli* were compared on toothbrushes stored in the laboratory. Toothbrushes can become contaminated through contact with the environment, and bacterial survival is affected by toothbrush storage containers. Dayoub *et al.* (1977) found that toothbrushes placed in closed containers and exposure to contaminated surfaces give higher bacterial counts than those left open to air. Mehta *et al*. (1990) found that the use of a cap for toothbrush storage increased bacteria survival. Increased humidity in the environment increases bacterial survival on toothbrushes and bacteria can survive for more than 24 hours in the presence of moisture. The persistence of viable *Staphylococci* on a drying toothbrush in the humid atmosphere of a toothbrush holder is not surprising; interventions such as chlorhexidine, toothpaste, mouthwash, and ultraviolet sanitizers cab however, reduce bacterial survival (Downes *et al.*, 2008).

Although sterile at birth, a great variety of microbes develops during the first day of life, including: *Streptococcus, Staphylococcus, Neisseria, Candida, Lactobacillus, Veillonella and* coliforms (McCarthy *et al.*, 1965; Socransky and Manganiello, 1971). Mutans *Streptococci* (MS), which is the primary etiological agent of human dental decay, is however, only found following dental eruption because it needs a hard surface on which to develop. Catalanotto (1975), Fujiwara (1991), Glass, (1992) and Glass and Lare (1996) showed that toothbrushes are

particularly relevant to the transmission of pathogens amongst immunocompromised patients, including coliforms picked up from the bathroom environment (Verran, 1996). While it is of course unlikely that toothbrushes will be intentionally shared amongst families and individual patients in hospitals, the potential still remains for accidental contamination-transfer. More importantly perhaps, is the fact that pathogens can re-infect patients from toothbrushes at the initial point when they are first immunocompromised and recycle pathogens, including MRSA. Toothbrushes are often exposed to sunlight and nearly always to drying –wetting cycles, all of which can reduce survivability. As a result, toothbrushes rapidly become contaminated with oral microbes, including caries causing pathogens like *Streptococcus mutans*, and opportunistic yeast pathogens like *Candida albicans* (Sammons *et al.*, 2004). Additionally, organisms not usually considered to be components of the oral microflora can frequently be isolated from toothbrushes, including Enterobacteria and pseudomonads. Toothbrushes can therefore be seen as a potential source of both oral and systemic infection and re-infection (Sammons *et al.*, 2004), particularly in immunocompromised patients and such organisms may also cause worrying medical problems in pregnant women (Bunete *et al.*, 2000). The aim of the work described in this section was to therefore to determine if household toothbrushes are contaminated with bacteria.

3.3 Influence of copper and plastic surfaces on the survival of bacteria in relation to the health care environment

3.3.1 Introduction

Metallic copper (Cu) surfaces have antimicrobial properties against a variety of different microorganisms and copper touch surfaces are likely to be increasingly used in public places including hospitals (Espírito Santo *et al.*, 2011). In recent hospital trials, non-Cu surfaces in frequent contact with both patients and staff were replaced with their Cu equivalents. The use of metallic Cu resulted in diminishing bacterial surface-loads of up to 90% as compared to no-copper controls (Espírito Santo *et al.*, 2011). Molecular mechanisms that result in rapid killing of Cu surface-exposed bacteria and yeasts were studied and shown to result from a sharp shock of extreme and immediate Cu-ion overload combined with severe membrane and cell envelope damage, although similar low mutation rates were observed in cells obtained from both Cu and control surfaces (Espirito Santo *et al.*, 2008; Quaranta *et al.*, 2011).

Mehtar *et al.*, (2008) conducted studies in which cells in buffer were applied to copper surfaces, incubated under ambient conditions, and were seen to be killed within hours, thereby mimicking contact of microbes to dry copper touch surfaces. Under such conditions, most microbes were found to be killed within minutes. Quaranta *et al.* (2011) found that copper ions are released from metallic copper upon contact with cells, a process which undoubtedly contributes to contact-

mediated killing. Extracellular supplementation with substances which are protective against oxidative stress (e.g. Catalase, superoxide dismutase, or mannitol, a hydroxyl radical quencher) increased the time needed to kill copper surface-exposed *E. coli* cells, indicating a role for this process in Cu-mediated killing.

3.3.2 Materials and Methods

Survival of bacteria on the surfaces of copper and plastic plumbing surfaces

The antibacterial activity of copper surfaces was determined by overlying suspensions of *Staphylococcus aureus* and *Escherichia coli* on copper surfaces. Two copper items were used; a copper pipe push-fit elbow 15mm, a copper pipe compression stop end, 15 mm and (as controls) a plastic pipe connector 22mm (all obtained locally from Wickes Building Supplies Ltd) (Figure 3.7). All copper pipes were sterilized by autoclaving (120˚C for 20 min), while the plastic pipes were sterilized using a 10% ethanol spray. Bacterial suspensions from colonies were prepared in sterile saline equal to McFarland 0.5 turbidity. The pipes were contaminated by transferring a 10 microliter volume of the bacterial suspension, and the inoculum was allowed to out-spread and dry itself under sterile conditions. The experiments were performed at 18-23°C and each assay was carried out in duplicate. Results were calculated after 20 days. The numbers of viable organisms in the suspension were determined by serial dilution and plating on to Nutrient Agar plates; the plates being incubated at 37°C for 48h.

Figure 3.7: Copper and plastic pipes used to evaluate the antibacterial activity of copper and plastic surfaces.

3.3.3 Results

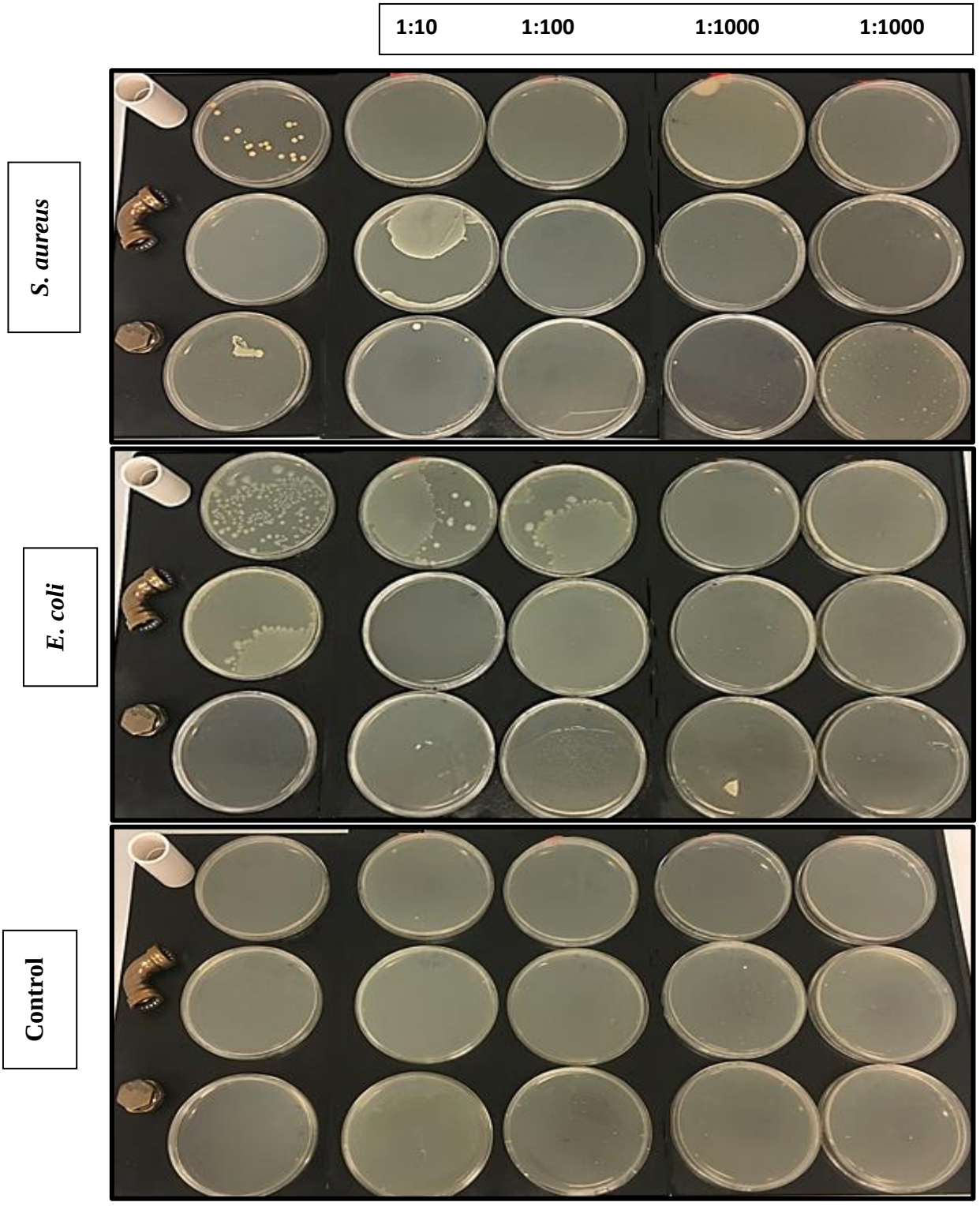


Figure 3.8: *S. aureus* and *E. coli* inoculated onto copper and plastic pipes.

Although copper and brass are traditionally used by UK plumbers for water pipes. in both hospitals and homes, they are gradually being replaced by plastic piping. It was of interest therefore to determine the survival of bacteria on both types of these surfaces. Copper is well known to be an antibacterial, and its use in medical environments is likely to lead to the continuous reduction of environmental microbial contamination, including MRSA. In viability assays, low counts of *Staphylococcus aureus* were seen on copper surfaces, as compared with those obtained on the plastic, control surfaces (Figure 3.8). The number of bacteria isolated from the plastic surfaces was consistently higher than the number isolated from copper surfaces. The survival rate of bacteria on the copper surfaces was low and none of the inoculated bacteria survived after 20 days of exposure. These results are similar to those found by Noyce *et al.* (2006) for copper, where survival was significantly lowered, with complete kill of MRSA being achieved after 90 min of exposure. Complete kills were produced on copper for all three strains of MRSA after 45, 60 and 90 min. The results presented here showed that *E. coli* failed to survive on copper pipes. These results are in agreement with those published by Wilks *et al.* (2005) who found that no viable *Escherichia coli* O157H7 were found on any of the copper pieces which they inoculated, even after only seventy-five to ninety minutes of exposure. Such results show that copper surfaces can remove cross contamination of pathogens in both households and health care settings and the continued replacement of other plumbing materials

with copper should minimize the risk of the survival and transmission of hospital-acquired infections.

3.3.4 Discussion

Copper has inadvertently been used as an antimicrobial agent for millennia, but its mode of action against microbes is still largely unknown. Today, nosocomial infections are a major health care threat and are responsible for large numbers of deaths and the resultant additional hospital costs, notably in the United States (Mehtar *et al.,* 2008). The effectiveness of copper an antimicrobial material is not restricted to bacteria as it also kills *Candida albicans* (and other pathogenic yeasts) which have emerged as important agents of hospital-acquired infections (HAI) (Mehtar *et al.,* 2008). Numerous studies have focused on the antimicrobial proprieties of copper (and its alloys) surfaces mainly in relation to the killing kinetics of a variety of microbial species exposed to different copper alloys. However, although it is becoming increasingly clear that metallic copper has excellent antimicrobial properties the molecular mode of action exerted by copper surfaces and the sensitivity of various cellular targets to its action are still largely unknown (Quaranta *et al.,* 2011). Studies have suggested a role for copper in ion homeostasis a factor in the survival of bacteria on copper surfaces. Cells of *Pseudomonas aeruginosa*, *Enterococcus hirae*, or *E. coli* which had their copper-ion defence systems deleted have been shown to die more rapidly than wild-type cells when exposed on metallic copper, although the survival times of mutants were not dramatically different from those of wild-type cells (Quaranta *et al.*,

2011). Mehtar *et al.*, (2008) reported that the minimum concentration of Cu to be an effective antimicrobial agent is > 55% for bacteria excluding *Mycobacterium tuberculosis* (MTB). Copper and its alloys showed a marked inhibitory effect on MTB, despite the strains being drug resistant. Growth of both strains showed inhibition by Cu (88–98% inhibition). The above mentioned work shows that the incorporation of Cu in healthcare facilities may dramatically help reduce the environmental microbial burden and act as a useful adjunct to current infection prevention and control systems.

3.3.4.1 Copper pipes

Although copper is a nutrient, when present in large amounts it becomes highly toxic is to organisms including hospital pathogens like MRSA. This effect is due to its ability to bring about the rapid fragmentation of a cell's DNA which leads to death; as a result, it is an effective biocide (Warnes *et al.,* 2010). As a result, it is obvious that, wherever possible, plumbing materials in health care settings should be made of copper. As we have seen, hand to hand transfer is the most important means by which microbes, including pathogens, are spread in hospitals. More generalized microbial contamination of the hospital environment also takes place (Noyce *et al.,* 2006) with the result that inanimate surfaces can act as a source of nosocomial infections largely because most Gram-positive and Gram-negative bacteria are able to survive for months on dry surfaces (Hota, 2004), and the main factors influencing the survival of microbes on dry surfaces include exposure to sunlight, humidity, and temperature (Kramer *et al.,* 2006).

Recently, considerable attention has been focused on revaluating metallic copper as a biocide for use in killing bacteria on so-called “touch surfaces”, which include door handles, bathroom materials, and metallic bed rails (Grass *et al.*, 2011). Weaver *et al*. (2010), for example, evaluated copper, as an alternative to alumium, as an antimicrobial surface for use in air-conditioning systems and this showed increased pathogen-killing by the former.

The copper content in copper alloys varies from 60% to 99.9%, and initial studies have shown that the survival rates of *E. coli* O157 vary considerably depending on the type of alloy used relative to its copper content (Noyce *et al.*, 2006). These authors noted a gene-mediated response in *P. aeruginosa* to survival on copper alloys and in *E. coli and E. faecium* strains increased resistance to copper ions was due to the presence of additional plasmid-borne copper resistance genes. It was noted that the greatest differences in survival rates were related to moisture content in the sample, the type of medium the bacteria were suspended in, and whether it was a Gram-negative or a Gram-positive bacterium. Since copper ion toxicity had been reported previously as a possible driving force in the contact-killing of *E. coli* on copper alloys (Espirito Santo *et al.*, 2008), an experiment was designed to block copper ions released from the copper surface by applying a corrosion inhibitor which would consequently prevent copper ions from entering the bacteria. This was correlated to electrochemical measurements and calculated concentrations of copper released from the surface, and an inverse relationship

was shown between the copper ion concentration released from the surface and survival rates of copper ion-resistant *E. coli*. Subsequently it has been shown that bacterial cells very quickly take up copper ions when exposed to copper surfaces which results in rapid cell death presumably related to increased oxidative stress (Grass *et al*., 2010; Espirito Santo *et al.*, 2011). Copper surfaces are now being tested in hospitals where their efficacy is compared to stainless steel touch surfaces for long term observation, isolation, and characterization of surviving microbes. However, bacteria will continue to acquire resistance and will continue to proliferate in nature due to pollution -exposure. Here copper resistance can be quite useful, such as in the bioremediation of copper mining wastes (Grass *et al.*, 2011).

CHAPTER 4

ISOLATION OF BACTERIA FROM USED TOOTHBRUSHES AND DETERMINATION OF THE ANTI BACTERIAL POTENTIAL OF TOOTHPASTES

4.1.1 Introduction

The oral cavity can be colonized by more than 700 microbial species, including fungi, viruses and a variety of unclassified microorganisms, most being commensal species that are beneficial for oral health. However, some are pathogens and can overcome the host responses and cause serious oral diseases. The oral microflora can be divided into two groups:

- **Saprophytes:** These are the permanent microflora of the oral cavity whose presence is needed for the normal functioning of the dental system, as well as the body in general. The saprophytic microflora affects the conditions of the local immune system, prevents the development of pathological conditions and supports the overall bacterial balance.
- **Pathogenic Microflora:** These affect the organs and tissues of the mouth and entire body and bring about the emergence and development of a variety of diseases. This microflora ideally should not be present, or present in very low numbers that fail to substantially affect the oral cavity and the body in general (Otoikhian and Okoror, 2012**)**.

An overload of pathogens in the oral microflora can result in caries, periodontitis and stomatitis, which are the most common oral microbial infections in humans. *Streptococcus spp*. and *Actinomyces spp*. are particularly common colonizers and cause supragingival plaque during the first stage of biofilm formation (Nascimento *et al.,* 2015). They also increase the acidity of the oral biofilm and thereby help to develop their cariogenic potential. After biofilm maturation, anaerobic and proteolytic bacteria, notably *Porphyromonas gingivalis, Tannerella forsythia, Treponema denticola* and *Fusobacterium spp.* are found to dominate the subgingival biofilm (Nascimento *et al.,* 2015).

Bacterial proteases and metabolic products often induce host responses like inflammation and immunoreactions which result in periodontitis/peri-implantitis. *Candida spp*. are the most common fungi in the oral cavity and often lead to denture stomatitis commonly isolated from infected root canals; additionally, they can act as opportunists in the formation of periodontal and peri-implantar lesions (Nascimento *et al.,* 2015).

Toothbrushes generally become highly contaminated with microorganisms which may arise from the oral cavity and from the environment in which toothbrushes are stored. As a result, toothbrushes may play a significant role in disease transmission and lead to an increase in infection risk (Frazelle and Munro, 2012). They act as a reservoir for microorganisms in both healthy and ill adults and contamination and survival of infectious organisms may occur on both animate and inanimate objects. Contamination of toothbrushes occurs after first use and increases with repeated

use and they can become contaminated from a variety of routes including: the oral cavity, environment, hands, aerosol contamination, and storage containers. Bacteria may become attached to and accumulate and survive on toothbrushes which may transmit individual disease causing organisms (Frazelle and Munro, 2012).

There is a clear correlation between contaminated toothbrushes and the presence of diseases (Glass and Lare, 1986), and changing a toothbrush regularly has been linked to the elimination of symptoms and disease regardless of its nature. Moisture is an obvious factor in promoting the survival of bacteria on toothbrushes and immunocompromised patients are at particular risk from their use.

4.1.2. Materials and Methods

Fifty toothbrushes were collected from volunteers aged 5 to 45 years. The toothbrushes were transported to the laboratory in a sterile polythene bag sealed with a rubber band. Brushes were processed within 12h by a method modified from that described by Sammons *et al*. (2004). The handle was cut off using a rotary saw and the head of the brush was retained in the bag to avoid contamination. Each brush head was then subjected to soaking in 10 ml of sterile water, for 20 min, followed by vigorous vortex mixing for 1 min and manual swabbing to dislodge persistently adherent bacteria. The resulting bacterial suspension was serially diluted and 0.1 ml aliquots plated onto nutrient agar to

select for bacteria. Plates were incubated aerobically at 37°C for 24–48 h. Total viable counts were estimated from the numbers of colonies on nutrient agar plates. Colony colour, morphology and haemolysis were recorded and Gram's stain was performed on a representative of each colony morphotype. Extraction of genomic DNA was by using KeyPrep bacterial DNA extraction kit supplied by ANACHEM. Test sample preparation for PCR, DNA quantification, polymerase chain reaction (PCR), agarose gel electrophoresis and phylogenetic analysis, has been explained above**.**

4.1.3. Results

1) Isolation of bacteria from various used manual toothbrushes by cultivation on Nutrient Agar medium

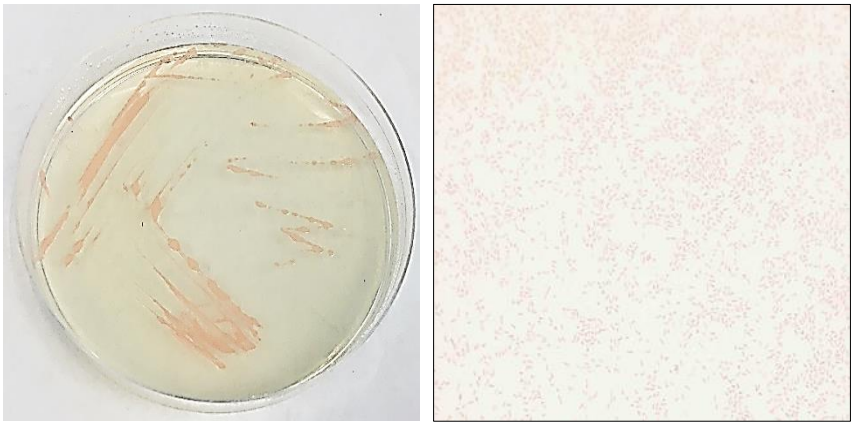
Bacteria were cultured using Nutrient Agar after isolation from used toothbrushes.

Table 4.1: Bacteria isolated from various used toothbrushes.

Representative sequence	Closest matches identification	Sequence identity	NBCI (Accession number)
1 TB	*Roseomonas mucosa*	99%	KF247232.1
2 TB	*Stenotrophomonas maltophilia*	99%	LN890169.1
3 TB	*Pseudomonas aeruginosa*	99%	KR815846.1
5 TB	*Leclercia adecarboxylata*	99%	KT899848.1
6 TB	*Enterobacter asburiae*	99%	EU239468.1
7 TB	*Candidatus Roseomonas massiliae*	99%	KT321690.1
8 TB	*Pseudomonas parafulva*	99%	KT758848.1
9 TB	*Bacillus licheniformis*	99%	KU314515.1
11 TB	*Pseudomonas aeruginosa*	99%	KF680991.1
13 TB	*Agrobacterium larrymoorei*	99%	EF178437.1
15 TB	*Pantoea septica*	99%	KF475883.1
16 TB	*Stenotrophomomnas rhizophila*	99%	KP050794.1
18 TB	*Citrobacter freundii*	87%	CP007557
20 TB	*Pseudomonas frederiksbergensis*	99%	EU373369.1

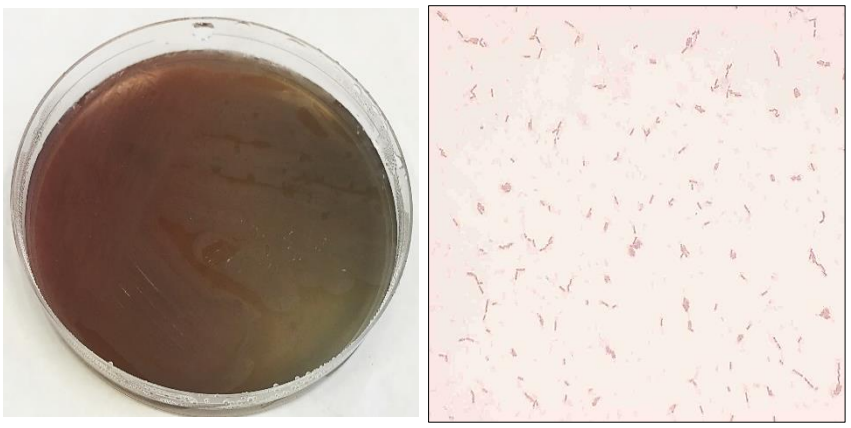
2) Light microscope images.

The isolates were examined under a light microscope after the bacteria were identified. (Figure 4.1)

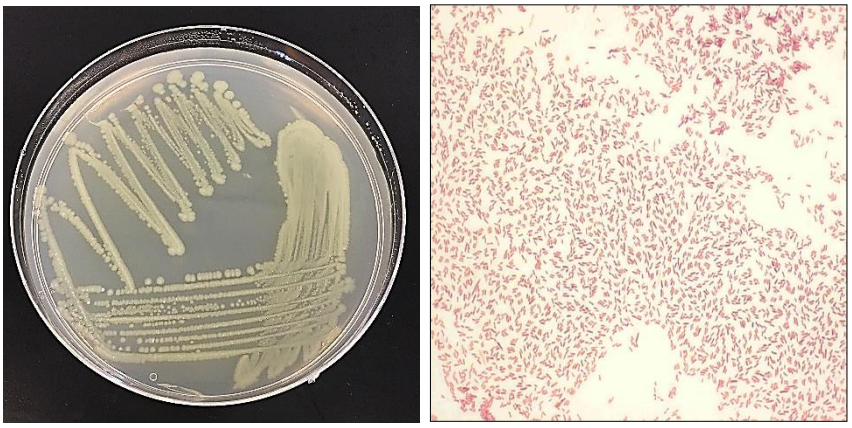


Roseomonas mucosa KF247232.1
Gram stained. Magnification: 100x.

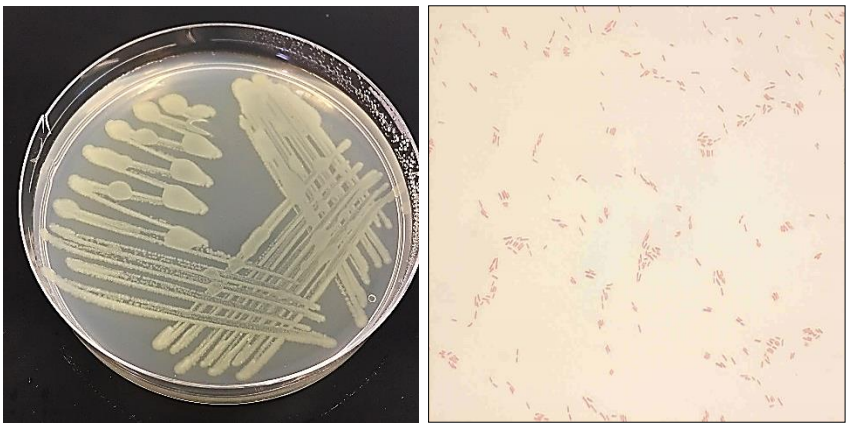
Stenotrophomonas maltophilia LN890169.1
Gram stained. Magnification: 100x.



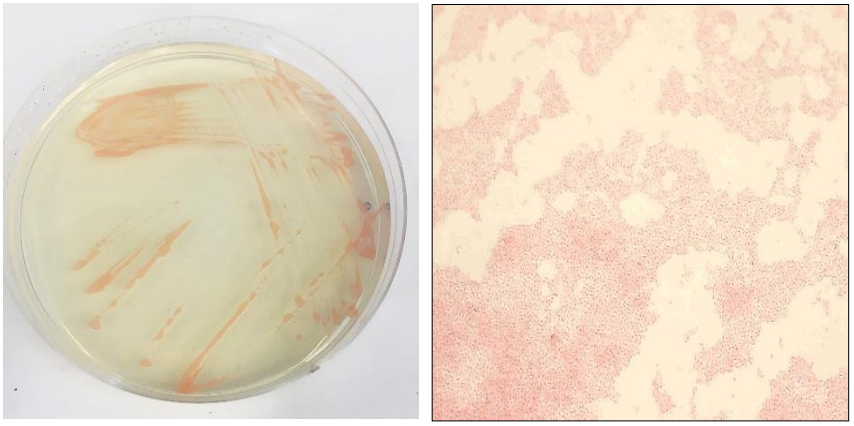
Pseudomonas aeruginosa KR815846.1
Gram stained. Magnification: 100x.



Leclercia adecarboxylata KT899848.1
Gram stained. Magnification: 100x.

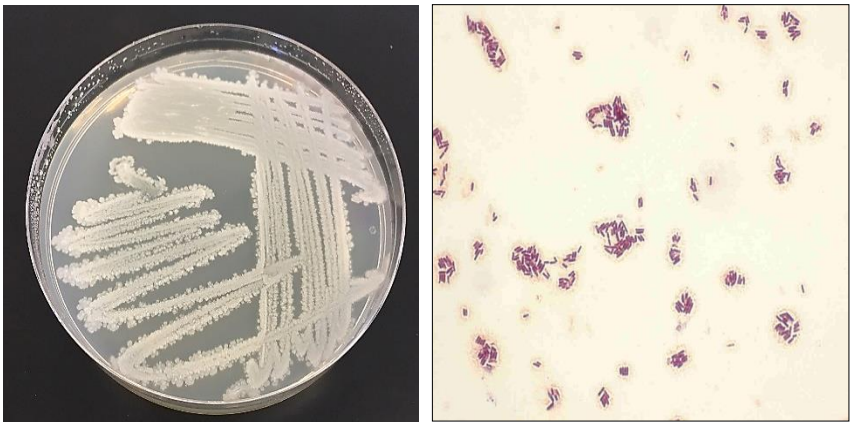


Enterobacter asburiae EU239468.1
Gram stained. Magnification: 100x.

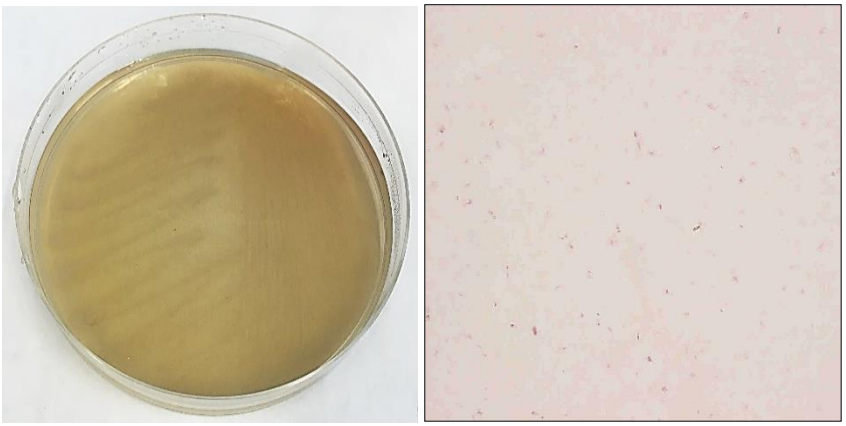


Candidatus roseomonas massiliae KT321690.1
Gram stained. Magnification: 100x.

Pseudomonas parafulva KT758848.1
Gram stained. Magnification: 100x.

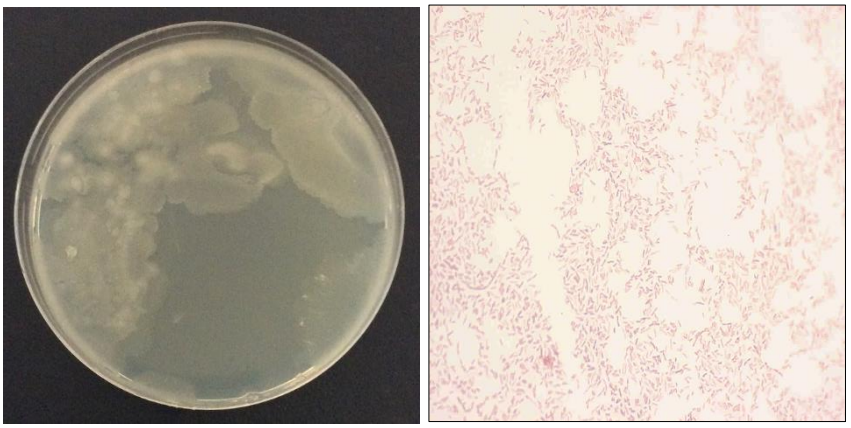


Bacillus licheniformis KU314515.1
Gram stained. Magnification: 100x.



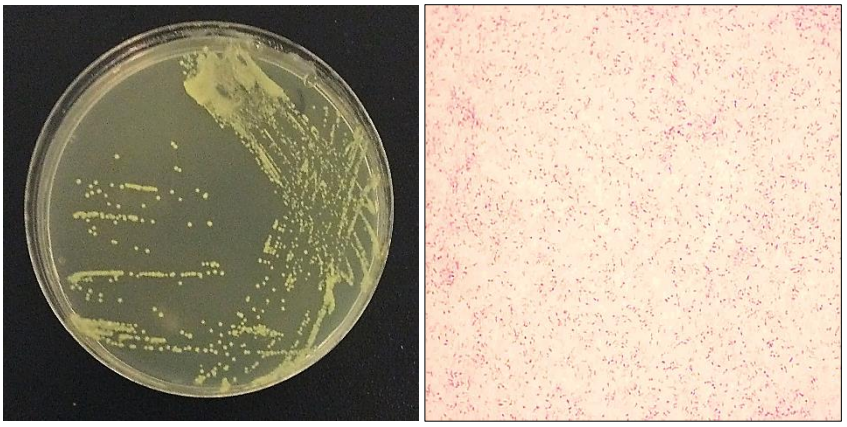
Pseudomonas aeruginosa KF680991.1
Gram stained. Magnification: 100x.

Agrobacterium larrymoorei EF178437.1
Gram stained. Magnification: 100x.

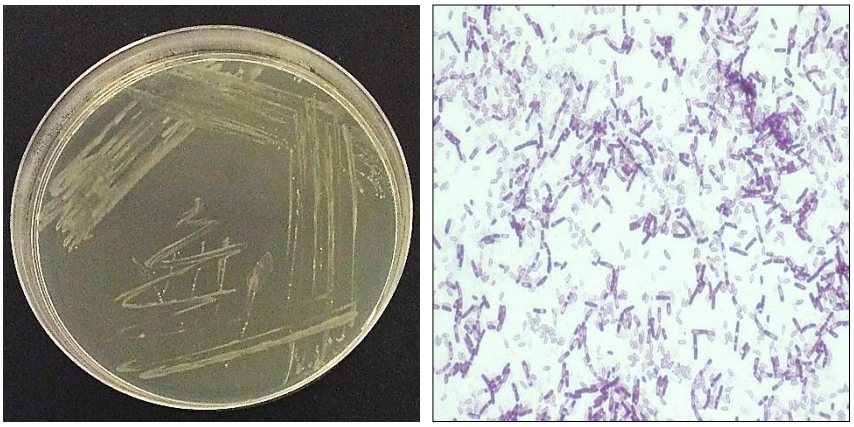


Pantoea septica KF475883.1

Gram stained. Magnification: 100x.



Stenotrophomomans rhizophila KP050794.1
Gram stained. Magnification: 100x.



Citrobacter freundii KP050794.1
Gram stained. Magnification: 100x.

Pseudomonas frederiksbergensis EU373369.1
Gram stained. Magnification: 100x.

Figure 4.1: Nutrient Agar plates showing cultured bacteria isolated from various used toothbrushes, and also microscopy images showing the bacteria under the light microscope.

Enterobacter asburiae

This bacterium is Gram-negative, non-motile and known to cause necrotizing fasciitis and pneumonia. Some *E. asburiae* isolates are identified as human pathogens which are an opportunistic pathogen and causes different human diseases such as community-acquired pneumonia, soft tissue infections, wound infection and other infections (Brenner *et al.*,1986).

Pseudomonas aeruginosa

Pseudomonas spp., notably *P. aeruginosa,* act as opportunistic pathogens particularly of the lower respiratory tract, bloodstream, and urinary tract amongst patients in intensive care units or which are immunocompromised. It is often isolated from moist areas within health care environments, such as taps, toilets, showers, respiratory equipment, and cleaning solutions. Skin, throat, and faecal carriage amongst healthy individuals have also been reported (Liu, 2011).

Pseudomonas parafulva

It is a Gram-negative environmental bacterium, frequently isolated from rice paddies. Colonies on nutrient agar were smooth, entire, and flat to convex and had a water-insoluble yellow pigment after an incubation of 24h at 35°C. This bacterium rarely causes acute meningitis (Ramirez *et al.*, 2010).

Pseudomonas frederiksbergensis

This bacterium is an environmental organism of no known pathogenicity.

Roseomonas mucosa

Roseomonas species are a recently typified group of pink, slimy, waterborne, Gram-negative coccobacilli. They typically cause fever associated with persistent catheter colonization, and *R. mucosa* has been isolated from various clinical samples, including blood samples, samples obtained from wounds, and samples obtained from the aquatic environment (Bard *et al.*, 2010).

Stenotrophomomas maltophilia

This bacterium frequently colonizes damp surfaces such as tubes used in mechanical ventilation, endoscopes, indwelling urinary and suction catheters. In immunocompetent patients, *S. maltophilia* is a relatively rare cause of pneumonia, urinary tract infection, or bloodstream infection; however, is a growing source of latent pulmonary infections. *S. maltophilia* colonization of with cystic fibrosis patients has been seen to be increasing (Brooke, 2012).

Stenotrophomomas rhizophilia

This is a soil and rhizosphere organism of no known pathogenicity. Cells are straight or slightly curved yellowish rods. Strains are plant associated and isolated

from the rhizosphere of oilseed rape and from the rhizosphere and tubers of potato (Wolf *et al.*, 2002).

Leclercia adecarboylata

L. adecarboxylata is a motile, Gram-negative rod. It is considered as the sole pathogen causing infection in an immunocompromised woman (Hess *et al*, 2008). It is considered as normal flora in the gut of animals and it has been isolated from human stools, from the skin of an asymptomatic blood donor and from a variety of environmental sources and drinking water. *L. adecarboxylata* have the ability to infect a variety of bodily fluids; it has been cultured from blood, sputum, peritoneal fluid, urine, synovial fluid, gallbladder tissue, cardiac valve tissue and wounds often as a part of mixed microbial growth in immunocompetent hosts (Tam and Nayak, 2012).

Agrobacterium larrymoorei

This is a soil organism of no known pathogenicity.

Citrobacter freundii

Citrobacter freundii is a Gram-negative, motile, facultative anaerobic bacterium that appear as rods or coccobacilli. *C. freundii* is often the cause of significant opportunistic infections. Also, it has been associated with neonatal meningitis and brain abscesses and with nosocomial infections in the respiratory tract and causes

pancreatic pseudocyst after an acute necrotizing pancreatitis (Badger *et al.*, 1999). It has been distributed in water, soil, food and the intestinal tract of humans. Urinary tract infections (UTIs) caused by *Citrobacter* species have been described in bacterial urine isolates in adults (Metri *et al.*, 2013).

Candidatus roseomonas massiliae

This is an organism of no known pathogenicity.

Pantoea septica

Cells are Gram-negative, motile by peritrichous flagella. *Pantoea* species are recovered from humans and are opportunist pathogens associated with contaminated catheters and penetrating trauma. *Pantoea septica* referring to the septicaemia outbreak associated with these strains (Brady *et al.*, 2010).

4.1.4 Discussion

Tooth brushes can be heavily infected with microorganisms, especially Streptococci, within a day's use and a lack of toothbrush disinfection and care promotes the spread of such pathogens, thereby causing inflammation of the oral tissues (Badger *et al.*, 1999).

Out of the fifty toothbrushes used for this study, none was found to be uncontaminated with bacteria. *Pseudomonas* species were found on four of the fifty toothbrushes, *Stenotrophomomnas sp*. and *Bacillus sp*. were found also. A

wide variety of bacteria belonging to different species were isolated from the investigated toothbrushes (Table 4.1).

Contaminated toothbrushes are recognized as a mode for microbial transport, and growth, and can result in the reinfection of a person with pathogenic bacteria or environmental microorganisms. The head area of tooth brush is prone to heavy contamination as fluids and food particles can be drawn by capillary action into the spaces between tufts, a process which may lead to bacterial growth (Frazelle and Munro, 2012).

4.2. Scanning electron microscope studies of the surface of a used toothbrush

4.2.1 Materials and Methods

Scanning electron microscope studies were conducted on the surface of bristles of tooth brushes undergoing normal use. A toothbrush used by the same individual for 6 weeks (alternating night and morning) was processed for scanning electron microscopy (SEM). Bacteria were fixed by immersing the brush head in 2.5% glutaraldehyde in 0.1 M sodium cacodylate buffer, pH7.3, for 60min. Brushes were rinsed in the same buffer, dehydrated in ethanol and critical point dried using liquid CO_2. A segment of brush head with one row of bristles was cut using a rotary saw, mounted on aluminium stubs, gold sputter coated and examined using a JEOL JSM-5300lv scanning electron microscope at an accelerating voltage of 10–30 kV (Sammons *et al.*, 2004).

4.2.2 Results and Discussion

Scanning electron microscopy of biofilms on toothbrushes used for approximately 3 months showed collections of cocci and the development of biofilms on the heads and bristles of both (Figure 4.2). The bristles were rough, providing ample sites for trapping organisms. Examination of a brush that had been used for more than 3 months revealed a biofilm on the brush head. The biofilm showed on the surface of the head to be made up of a compacted community of microorganisms, including cocci, bacilli and filamentous organisms, together with cellular and other debris.

SEM is showed biofilms on the heads and bristles of both conventional brushes, showing that bacteria colonized and grew on them. The rough surfaces of the bristles provide ideal sites for the entrapment of microorganisms and later development of biofilms, whilst nutrients will tend to accumulate at the base of the bristles thereby favouring the development of biofilms. Most dental practitioners recommend that brushes be changed after 2–3 months and following any bout of illness. The example shown here, of a brush that had been used in excess of five months, showed that after such a long period of use, extensive biofilms consisting of mixed communities of organisms developed at the base of the bristles and extended into the head of the brush. This process which could lead to the formation of a reservoir of organisms which can act as a potential source of infection for any vulnerable patient (notably where immunocompromised) or act as a source of cross-infection.

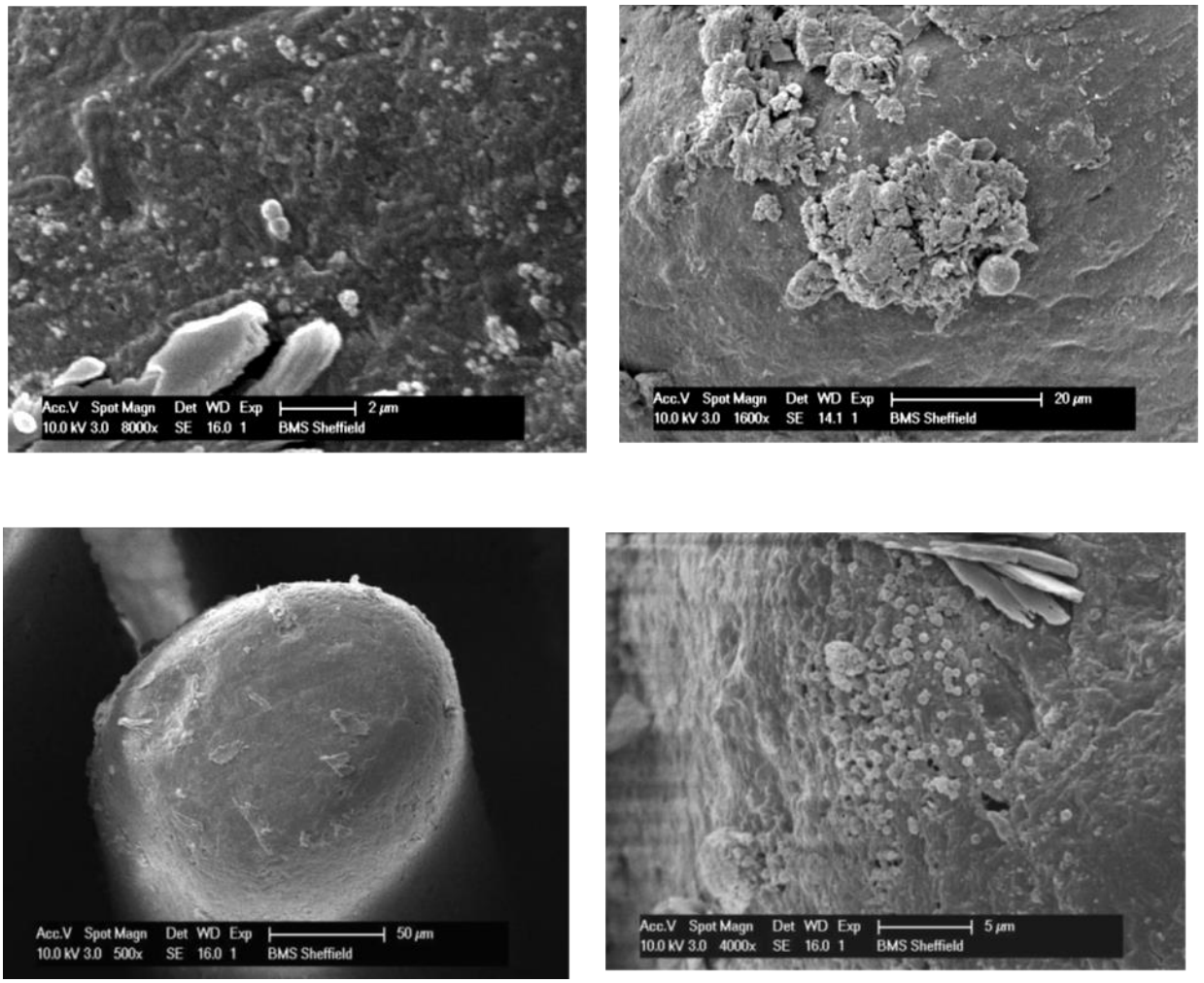


Figure (4.2): Scanning electron microscopy of toothbrush biofilms on antibacterial brushes used for approximately 3 months. Top left) showing debris and cocci bacteria 8000 ×, bar represents 2µm; top right) showing debris and biofilm; bottom left) image of tip of bristle, showing indentations and crevasses 500 ×, bar represents 50 µm; bottom right) cocci embedded in the biofilm, 4000 × bar represents 5 µm.

4.3. Effect of toothpastes on the bacterial growth

4.3.1 Introduction

Standard toothpastes are usually made up of a mix of fluoride and detergents both of which are generally thought to improve biofilm-control. Surprisingly, however, many toothpaste-based antimicrobials have yet to be effectively tested or proven to work in the oral environment.

Fluoride, in marketed dentifrice is usually comprised of sodium fluoride (NaF) which is a widely recognized anti-caries agent and NaF-containing oral hygiene products which significantly reduce dental caries (Barboza-Silva *et al.,* 2005). Fluoride inhibits a variety of bacterial processes which are meditated by enzyme binding (Barboza-Silva *et al.*, 2005). The main urease producers are *A. naeslundii* and *Staphylococcus epidermidis* while *S. epidermidis* is often the most ureolytically active organism present in plaque. Fluoride directly inhibits bacterial ureases (Barboza-Silva *et al*., 2005), while chlorhexidine is bacteriostatic and bactericidal against both Gram-positive and Gram-negative microbes (based on its ability to damage cytoplasmic membranes and disrupt cell membrane integrity). Microbial contamination can be effectively removed by immersing them on chlorhexidine overnight.

4.3.2. Materials and Methods

In order to determine the antibacterial effect of toothpastes (fluoride and chlorhexidine toothpastes) a toothpaste agar was used containing 100 ml bacteriological agar and 4 g of a proprietary toothpaste in 9 laboratory bottles. The

basal medium used for isolation and growth for bacteria was bacteriological agar which is composed of (g/l): 70% agarose and 30% agaropectin, final pH 5.7-7.0 at 33-36°C. Suspend 23 g of bacteriological agar in 1000 ml of distilled water. The bacteriological agar was boiled to dissolve the medium completely and sterilized by autoclaving at 15 lbs. pressure (121°C) for 15 minutes. The melted agar was poured in half of Petri plates and left them to be cool and set. For preparation the toothpaste agar: bacteriological agar 50 ml was dissolved in 9 Duran laboratory bottles and sterilized by autoclaving, then added 4 gram of Commercial toothpastes in the bottle (Figure 4.3). The bottles were shacked and vortexed at low speed until complete mixing was achieved. The mixed toothpaste agar was poured in the other half of plates and left them to be cool and set. The plates were streaked by model strains of *Staphylococcus aureus* and *Escherichia coli* in both sides of plates over the medium. All plates were incubated in the 37°C for 18-24 hours. After incubation, an ellipse of inhibition was used to determine the effect of toothpaste on growth of bacteria.

Figure 4.3: (left) The commercial toothpastes and (right) chlorhexidine toothpaste all used to prepare toothpaste agar plates.

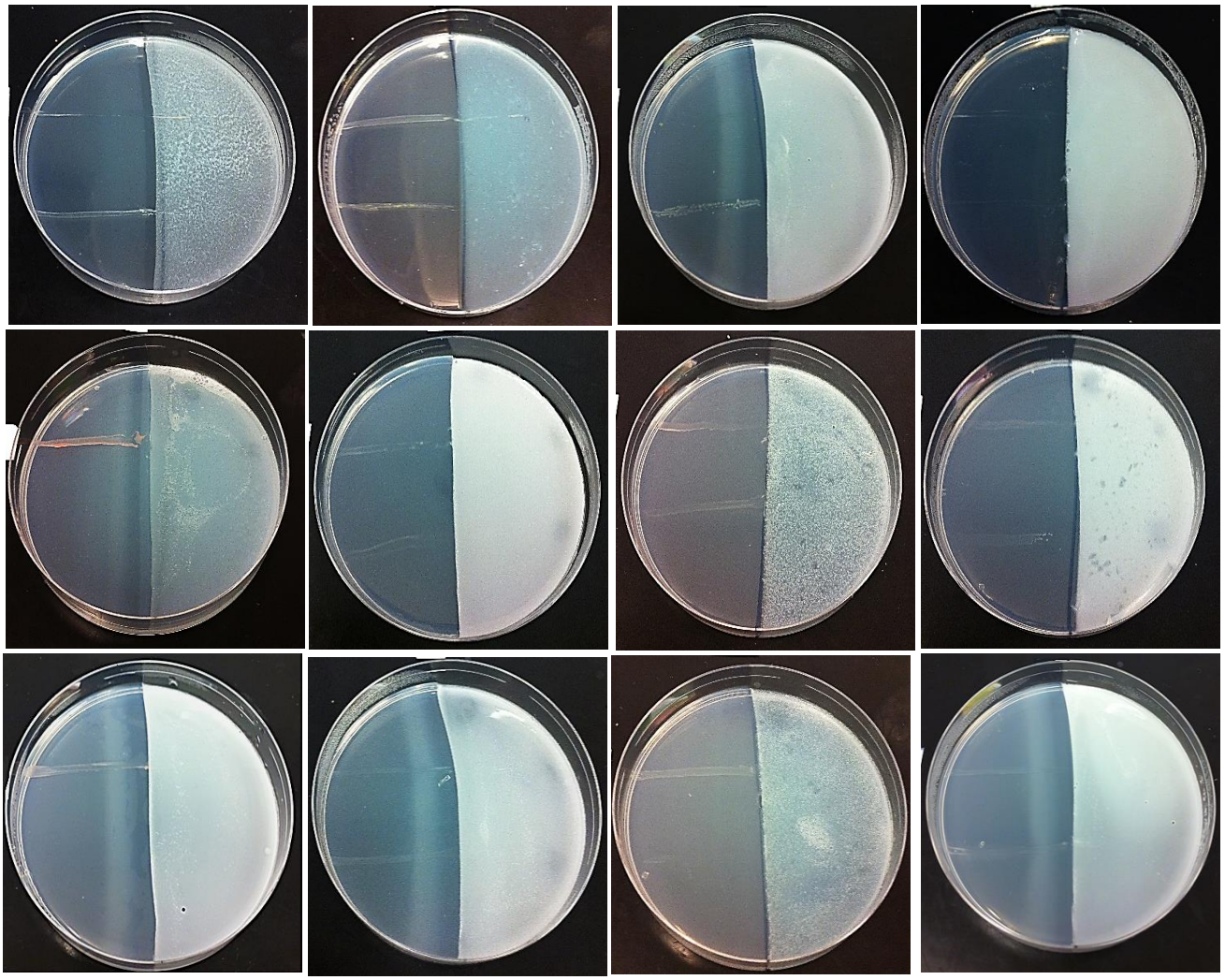


Figure (4.4 A) Half agar plates containing fluoride-containing commercial toothpastes inoculated with bacteria.

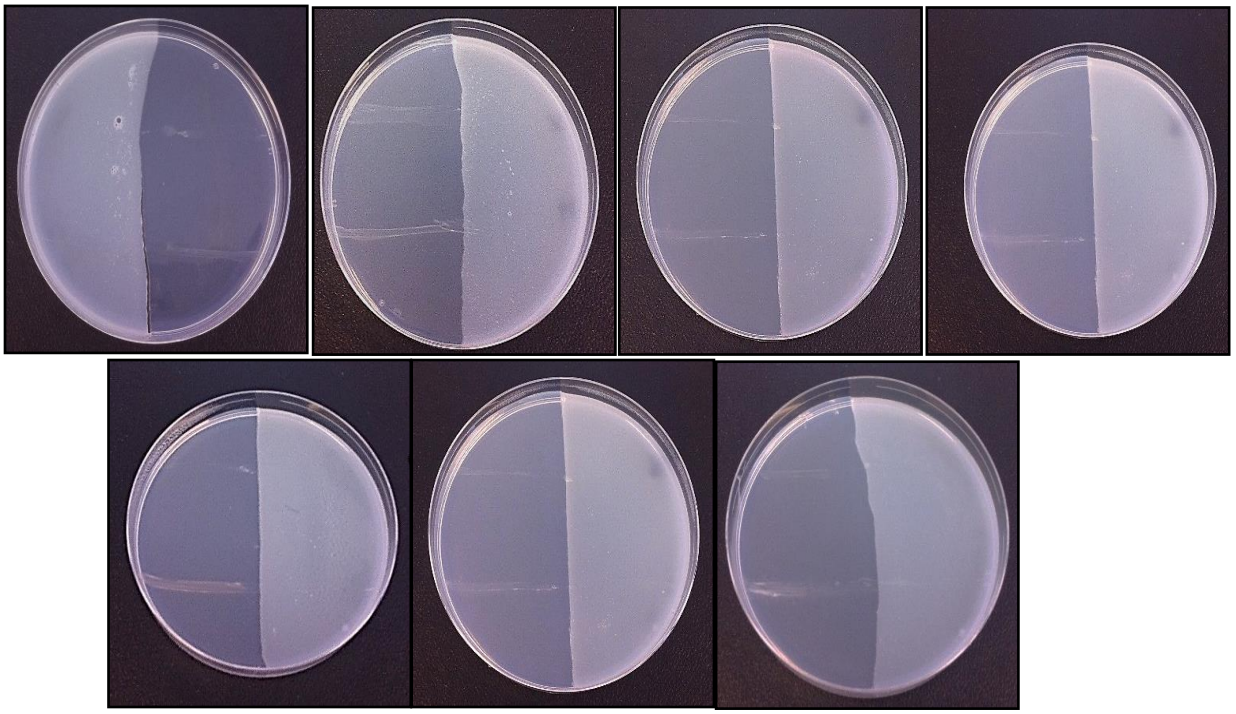


Figure (4.4 B) Half agar plates containing chlorohexidine commercial toothpastes inoculated with bacteria.

4.3.3. Results and Discussion

The results showed that the bacteria isolated from toothbrushes can grow on the agar only side, but no bacteria grew on the toothpaste-containing agar. This result proves that toothpaste acts as an antibacterial agent and can inhibit bacterial growth. The main reason for inhibition is the presence in toothpaste of fluoride which is widely used as an effective anti-caries agent (i.e. antibacterial) agent. Marquis (1995) showed that fluoride can affect bacterial carbohydrate metabolism and that it inhibits the functioning of essential bacterial enzymes; it also reduces the acid tolerance of bacteria and thereby prevents bacteria growth. Fluoridated

toothpastes showed antibacterial activity against *S. mutans* and both aerobic and anaerobic oral flora and also inhibited Streptococci selectively, and inhibited caries formation by interfering with biofilm development by Streptococci (Randall *et al.*, 2015).

Chlorhexidine toothpastes also inhibited bacterial growth when added to toothpaste agar plates. De Rossi *et al*. (2014), showed that chlorhexidine toothpastes presented antimicrobial activity against Gram-positive bacteria and yeasts and that the chlorhexidine molecule has both bactericidal and bacteriostatic antimicrobial effects on the tooth surface. In the present study, chlorhexidine was found to be effective in disinfecting contaminated toothbrushes, although in other studies Listerine was shown to be more effective. The higher efficacy of chlorhexidine could be due to its extended action-spectrum. It is also relatively non-toxic, odourless and is a commonly used mouthwash, properties which make chlorhexidine a good choice for the disinfection of contaminated toothbrushes.
In conclusion, the results presented in this Chapter show that all toothpastes exhibited effective antimicrobial activity against the tested bacteria and that these products were able to inhibit the growth of bacteria. In addition, adding chlorhexidine to dentifrices can result in effective antimicrobial activity against all the evaluated Gram-positive bacteria and yeasts. However, further studies are required to evaluate their clinical advantages in the treatment or prevention of biofilm-mediated diseases.

4.4 Discussion

Again, the importance of these isolates is not that they are major pathogens, but that they can infect immunocompromised patients (Ankola *et al.*, 2009). Toothbrushes get re-contaminated after each use (Frazelle and Muro, 2012) and such re-contamination of the oral cavity can result from the retention of microorganisms on toothbrushes (Filho *et al.*, 2000, Karibasappa *et al.*, 2011). Nascimento *et al.* (2012) showed that new toothbrushes may often carry bacteria even before their use, since no regulatory requirement for pre-use sterilization is generally required. This observation was confirmed in our study, where all (100%) of new tested brushes were contaminated positive for bacterial growth, a finding which explains the high incidence of *Bacillus cereus* and *Candida albicans* on toothbrushes and oral swabs.

The effectiveness of toothbrushes at cleaning, and bacterial plaque removal largely depends on their abrasive qualities, although some toothpastes also contain antibacterial agents (which are often general sterilants) such as hexachlorophene. Toothpastes also contain a combination of fluoride and detergents, compounds which increase their efficiancy (Davies, 2008; Marsh, 2010; Prasanth, 2011); triclosan for example, is a low-toxicity, non-ionic, chlorinated bisphenol that is compatible with toothpaste additives like fluoride and surfactants, and it enhances the inhibition of cyclooxygenase/lipoxygenase pathways and also exhibits anti-inflammatory properties (Davies, 2008; Davies *et al.*, 2010). Chlorhexidine is usually regard as the most effective antimicrobial agent for use in dentistry (Jones, 1997; Twetman, 2004). Its effectiveness is due to the dicationic nature of the

chlorhexidine molecule, which leaves a lasting antimicrobial effect on the tooth surface (Twetman, 2004). Compounds derived from plants also have useful antimicrobial properties which are relevant to toothpaste use (Verkaik, 2011; Pannuti, 2003). A toothpaste called Parodontax for example, is an herb-based product which contains sodium bicarbonate and a number of herbal extracts such as chamomile *Echinacea*s and *Mentha piperita* (Panuti, 2003). For obvious reasons, the use of easily utilizable sugars is avoided as additives to toothpastes, although carbon substances which can support microbial growth are always present in moist and dry sputum.

The results presented show that tooth brushes are contaminated with potentially pathogenic bacteria and that toothpastes act as a microbial nutrient source. As a result, it is highly desirable that only sterile, one time-use tooth brushes should be used by immunocompromised patients. Although modern toothpastes are generally free of readily utilizable sugars, they provide microbial substances in the form of dried sputum and food particles. The antibacterial effect of toothpastes was determined using a readily available family and thus the results showed that pathogenic bacteria failed to grow on bacteriological agar containing toothpastes. The most likely explanation for the inhibitory effect is that the bacteria were inhibited by fluorides which are added to toothpastes as anti-carries agents. Some toothpaste also contains more specific biocides which play a role, alongside

fluorides in inhibiting potentially pathogenic bacteria by inhibiting carbohydrate metabolism and inhibiting essential enzymes (Marquis, 1995).

CHAPTER 5

EFFECTIVENESS OF ANTIBACTERIAL CLOTHS IN INHIBITING THE GROWTH OF BACTERIA

5.1 Introduction

The silver ion has long been known to be effective in inhibiting or killing a broad range of microorganisms and silver is increasingly being used to control bacterial growth in a variety of medical applications, including dental work, catheters, and in the healing of burn wounds (Jung *et al.*, 2008). Slow-release "nanosilver" linings are also used in laundry machines, dishwashers, refrigerators, and toilet seats. The mechanism of the antimicrobial action of the silver ion relates to its interaction with thiol (sulfhydryl) groups. Amino acids, such as cysteine, and other compounds containing thiol groups, such as sodium thioglycolate, neutralize the activity of silver against bacteria (Jung *et al.*, 2008). Silver affects bacterial enzymes and brings about a marked inhibition of bacterial growth with elemental silver often being deposited in the vacuole and cell wall as granules. This element also inhibits cell division, damages the cell envelope, and can denature the contents of the bacterial cell (Jung *et al.,* 2008). Under the influence of silver ions, bacterial cells increase in size, and the cytoplasmic membrane, cytoplasmic contents, and outer cell layers all exhibit structural abnormalities. Finally, silver ions interact with nucleic acids and interact preferentially with the bases in DNA rather than with the phosphate groups (Jung *et al.,* 2008).

5.2 Materials and Methods

The aim of the following experiments was to determine the effect of antibacterial e-cloth (EnivroProducts Kent, TN3 8LE) and a control microfiber cleaning cloth on bacterial contamination (Figure 5.1).

Two types of silver impregnated cloths (antibacterial e-cloth “red colour” and a non-antibacterial microfiber cleaning cloth “yellow colour”) were applied to environmental surfaces (desks, air conditioner, windows, medical equipment, laboratories). Pieces of cloth were moistened with sterile water and wiped firmly over the entire surfaces. Two approaches were used. In the first method, silver containing cloths were used for isolation of various bacterial contaminants from environmental surfaces. Sterile water moistened pieces of cloths were wiped firmly over the entire surfaces. Half the number of cloth was placed in 50 ml of Nutrient broth in sterile tubes, and vortexed for one minute and was left in the shaker for overnight. After 18-24 hours of inoculation, the Nutrient Broth medium became turbid, the turbidity ensuring the presence of certain bacteria in the samples. The other half was placed on the surface of nutrient agar plates and the plates left in the incubator for 18-24 hour. After incubation, the presence or absence of bacterial growth was noted. For morphological identification of bacterial colonies, different types of bacterial colonies appeared on the Nutrient agar plates. Pure colonies of isolates were identified and characterized using standard microbiological techniques. The second method involved using silver containing cloths to determine the effect of silver as an antimicrobial on growth of

bacteria. Sterile water moistened some cloths were placed on the centre of the medium and streaked with cultures of *Staphylococcus aureus* and *Escherichia coli* (i.e. on both sides adjacent to the cloth). These plates were incubated at 37°C for 18-24 hours. Sterile water moistened cloths were placed on the centre of the Sabouraud Dextrose agar plates and streaked with cultures of *Candida inconspicua* and *Candid rugose* then incubated at 25°C for 5 days. After incubation, the size of any resultant inhibition zone was measured.

Figure 5.1: A) The antibacterial e-cloths and B) non-antibacterial microfiber cleaning cloths.

5.3. Results

5.3.1: Isolation of various bacterial contaminants from environmental surfaces using silver containing cloths on nutrient agar plates and nutrient broth.

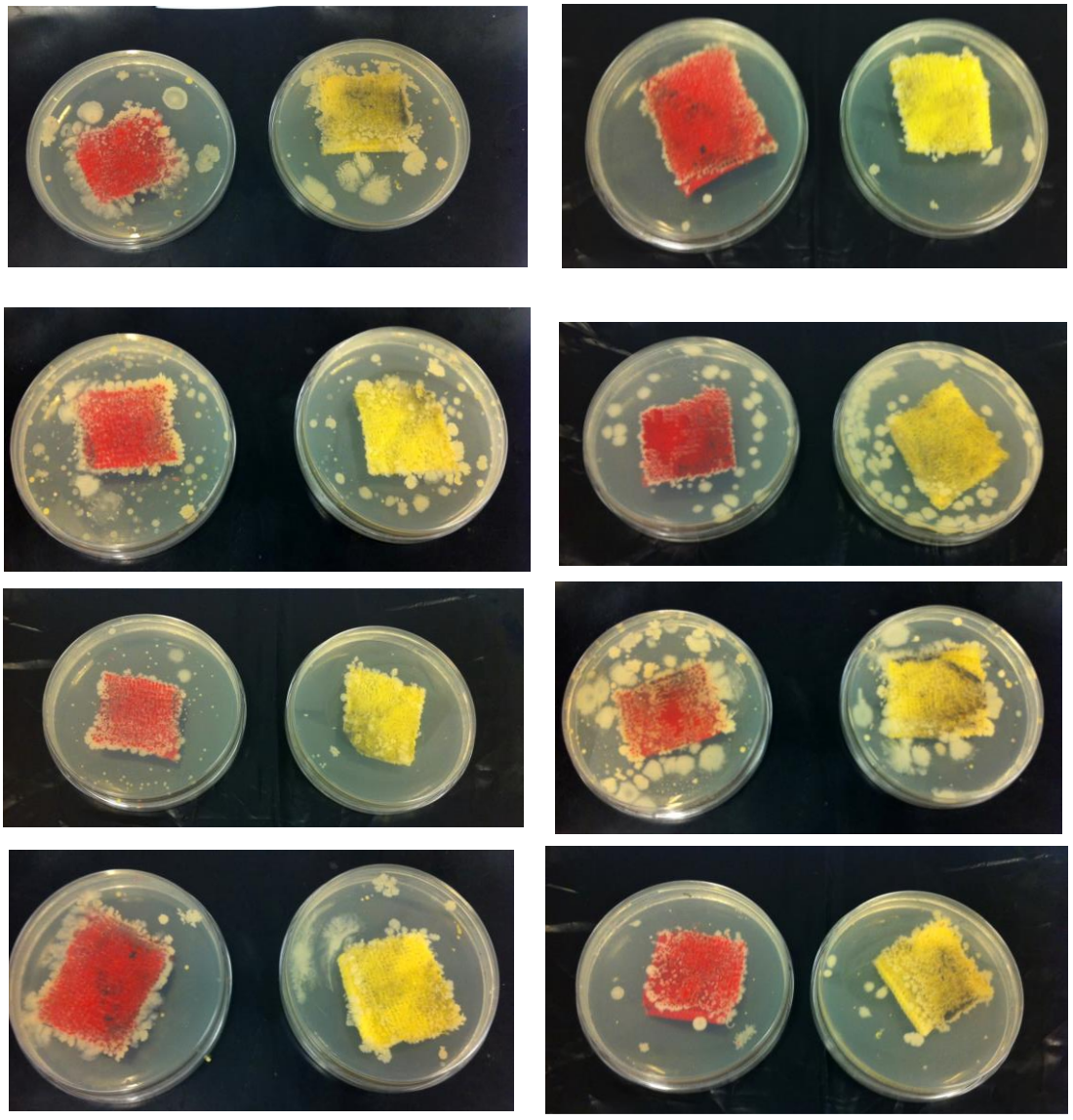


Figure 5.2: Bacterial growth around the antibacterial and control cloth pieces after isolation from different surfaces.

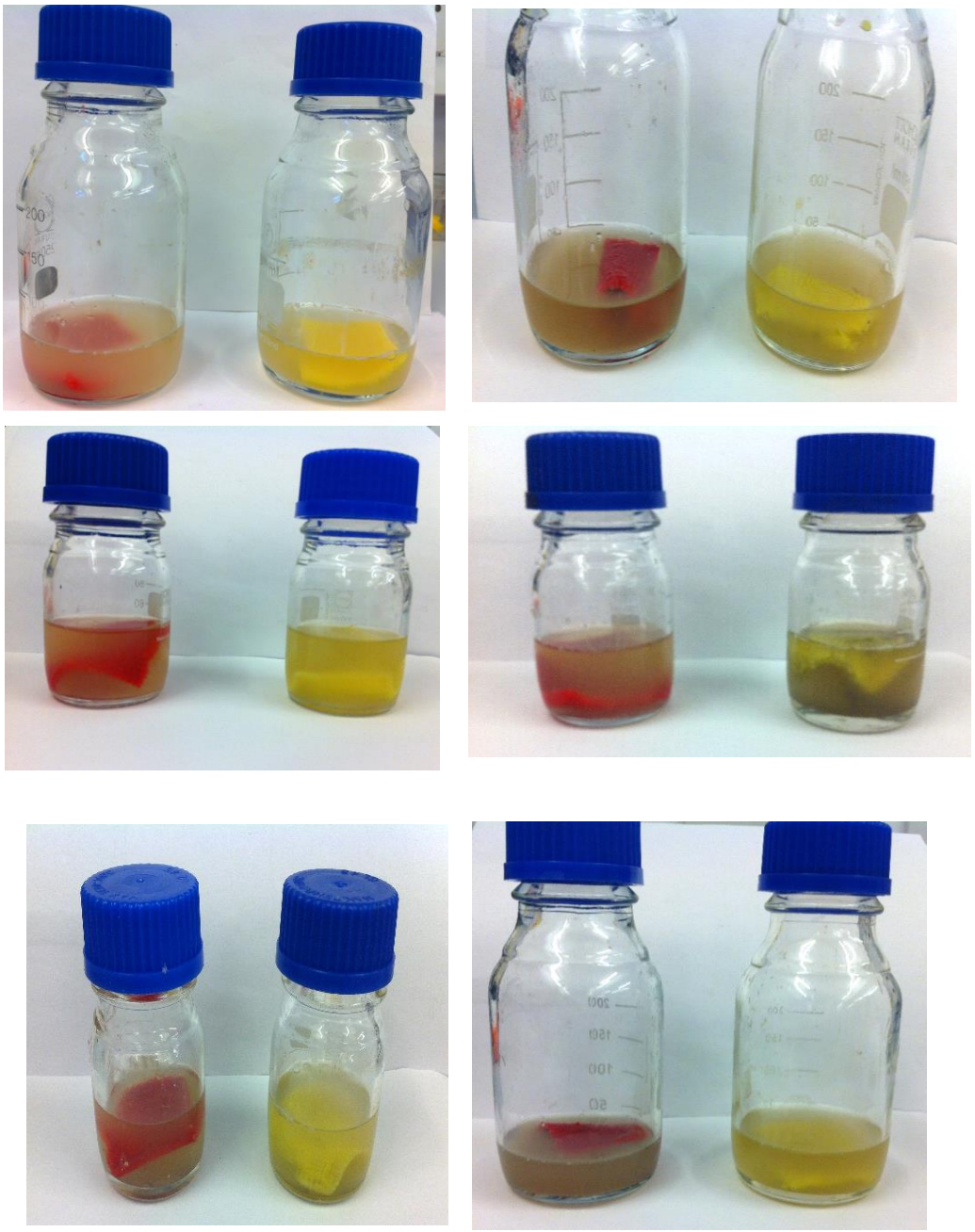


Figure 5.3: Growth of bacteria in the nutrient broth inoculated with the antibacterial and control cloths pieces after isolation from different surfaces.

5.3.2 Examination of the effect of silver as an antimicrobial on growth of bacteria

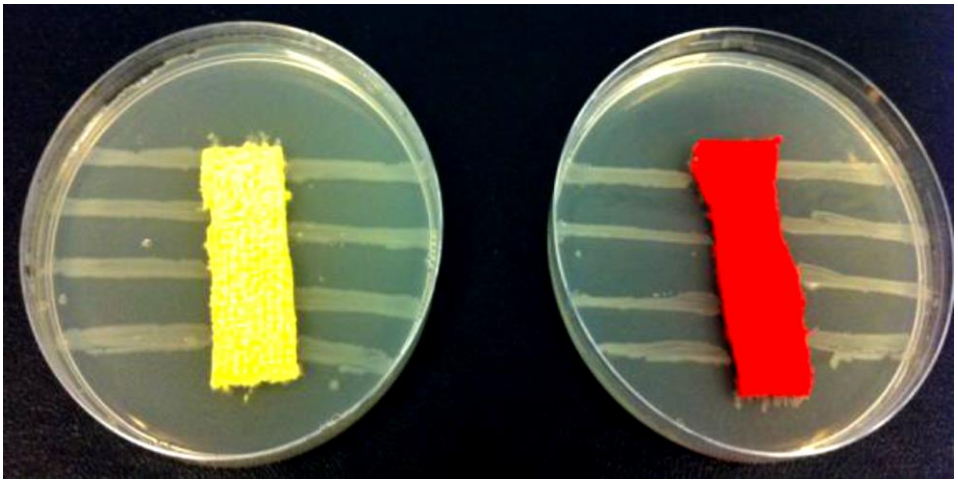


Figure 5.4: No inhibition zones appeared around the antibacterial cloths and the control. The bacteria strain used is *E. coli*; yellow is the control cloth and red is the tested antibacterial cloth.

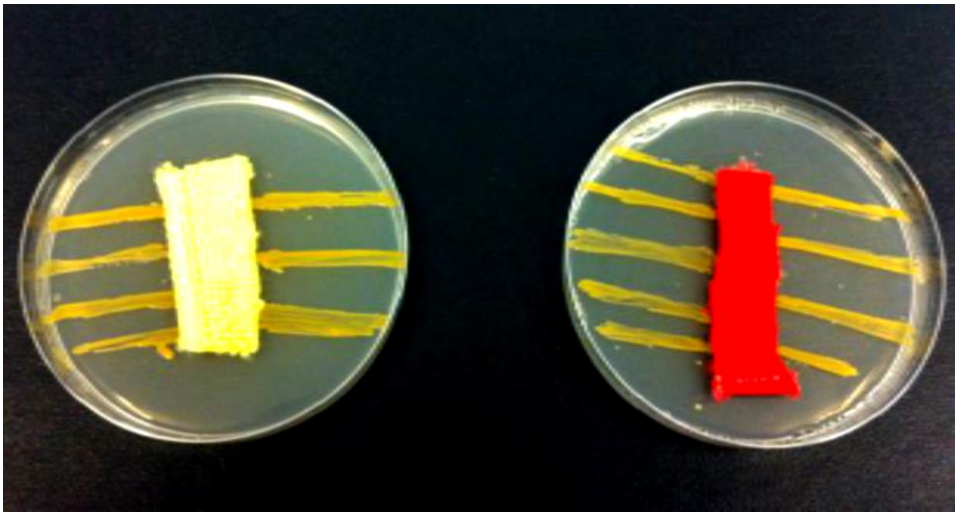


Figure 5.5: No inhibition zones appeared around the antibacterial cloths and the control. The bacteria strain used is *S. aureus*; yellow is the control cloth and red is the tested antibacterial cloth.

5.3.3 Examination of the effect of silver as an antimicrobial on growth of *Candida sp*.

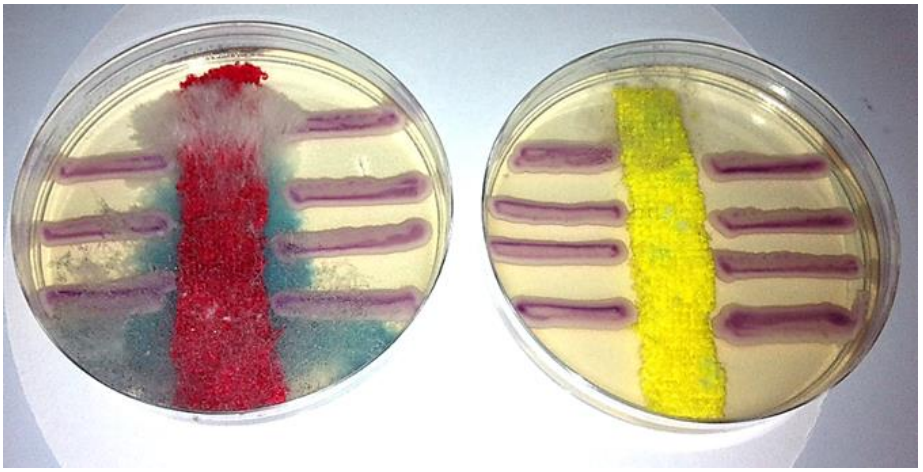


Figure 5.6: No inhibition zones appeared around the antibacterial cloths and the control. The fungal strain used is *Candida inconspicua*; yellow is the control cloth and red is the tested antibacterial cloth.

Figure 5.7: No inhibition zones appeared around the antibacterial cloths and the control. The fungal strain used is *Candida rugose*; yellow is the control cloth and red is the tested antibacterial cloth.

5.4. Discussion

The antibacterial effects of silver containing cloths against bacteria was determined using two techniques with two types of cloths, one an antibacterial cloth containing silver and a non-antibacterial cloth as control. The first method indicated that the growth of bacteria was heavy and there was no effect of silver on bacteria growth. There was no significant difference between the growth resulting from cloths containing silver and control cloths. Both showed the same results (Figure 5.2, 5.3). The bacterial growth was not affected by bactericidal activity resulting from silver.

The silver impregnated cloth used here was wiped on various surfaces and, not surprisingly, became contaminated with dust and dirt and, when this was transferred to growth medium, it supported bacterial growth. The antibacterial cloth did not prevent the growth of bacteria when incubated adjacent to the organisms on a solid growth medium. This result is entirely unexpected, since the cloth used here is marketed as an antibacterial material based on its silver content and its claimed ability to act as a broad spectrum micro-biocide capable of inhibiting bacteria and fungi including MRSA, and other antibiotic resistant species (Gupta and Chauhan, 2016). It is likely that the concentration of silver present in the cloth is too low to be capable of inhibiting bacteria and it appears that the antibacterial cloth, used here, would be of little use for controlling pathogens on surfaces in household and hospital settings.

The second method showed that no inhibition zones appeared around the antibacterial cloths, so the growth of bacteria was not affected by the sliver on cloths as shown in (Fig 5.4 ,5.5). Also, the antibacterial cloth did not prevent the growth of two yeasts when they were incubated adjacent to the material on a solid medium (Figure 5.6, 5.7). This result is both surprising and worrying, since it shows that cloths which are advertised and sold to kill bacteria do not do so. The result may be due, however, to the fact that heavy bacterial loads were used in this study. Further work will continue using lower loads.

It is known that the enhanced antibacterial effect of nanoparticles is due to their large surface to volume ratio, and therefore the smaller the particle, the greater this effect would be. Yu *et al.* (2013) reported that nanocomposites of larger sized AgNPs were much less cytotoxic than the smaller ones, without sacrificing the antibacterial potency of smaller particles.

The mechanism behind the antimicrobial potency of Ag nanoparticles is still not clear. It is believed that their antibacterial efficacy could stem from their absorption by bacterial cells, resulting in the shrinkage of the cytoplasmic membrane (Pattabi *et al.*, 2013). An alternate mechanism proposes that due to the interaction of Ag ions with the S-H bonds in proteins, the DNA loses its capacity to replicate and proteins become deactivated (Pattabi *et al*., 2013).

CHAPTER 6

SURVIVAL AND RELEVANT METABOLIC DIVERSITY OF ISOLATES

6.1 Introduction

Bacteria play a major role in the cycling of elements in the outdoor and built environments, being involved in all of the major cycles, including participating in transformations of C, N, P, S as well as modifying elements such as copper, manganese and iron (Killham,1994). The aim of the work reported below was to determine the ability of some of the bacterial isolates to hydrolyse urea, nitrify, oxidize reduced form of sulphur, solubilize insoluble phosphate and oxidise copper and iron sulphides. Some of these transformations are particularly relevant to healthcare environments, such as the hydrolysis of urea (present in urine) or the oxidation of copper and iron sulphides which are found in corroded hospital, metal pipes. Other transformations, such as the formation of thiosulphate may also enable bacteria to better survive in the medical environment by protecting them from the toxic effects of, for example, heavy metals, or even possibly biocides. The following is a brief survey of the transformations which occur in mineral cycling which are relevant to the work described here. Further details on these transformations can be found in the following references: Alexander (1977), Maier *et al.* (2009), Killham (1994) and Paul and Clark (1989).

Urea hydrolysis: Urea is water soluble and has a high nitrogen content exceeding that of ammonium nitrate and ammonium sulphate. Microbes secrete

ureases which converted urea to carbon dioxide and ammonia. A wide range of bacteria can mediate this process including species of *Pseudomona*s, *Achromobacter, Bacillus* and *Micrococcus.*

Nitrification: Nitrification is of major importance for the N-cycle in aquatic and terrestrial environments. It involves the oxidation of ammonium (NH_4^+) to nitrite (NO_2^-) and then nitrite to nitrate (NO_3^-) by chemoautotrophic bacteria and by some heterotrophic fungi and bacteria, which can also perform these oxidations. Two kinds of nitrification exist (Killham, 1994): The first involves the activity of chemoautotrophic nitrifying bacteria (*Nitrosomonas)* by which ammonia (NH_3) or ammonium (NH_4^+) ions are oxidised to nitrite (NO_2^-). The second part of the process involves chemoautotrophic Gram-negative bacteria which oxidize nitrite (NO_2^-) to nitrate (NO_3^-). *Nitrobacter* and some fungi such as species of *Penicillium* and most other *Deuteromycetes* can also perform these oxidations (Maier *et al*., 2009).

Sulphur oxidation: Sulphur is an essential element for growth of all organisms, being a required element for the synthesis of the amino acids, cysteine and methionine, and vitamins such as vitamin B1 (thiamine), hormones such as biotin, coenzymes and lipoic acid. Filamentous fungi play a role in the S- cycle; for example, *Fusarium solani* (a soil fungus) oxidizes elemental sulphur to polythionates, thiosulphate and sulphate. Fungi oxidize sulphur to sulphate with the formation of tetrathionate and thiosulphate. These products, it has been

suggested, may protect fungi from the toxic effects of heavy metals (Alexander, 1977).

Phosphorus solubilisation: Bacteria and fungi are able to solubilise phosphate and release P when growing *in vitro* with calcium phosphate, apatite or other sources of insoluble phosphate; phosphate solubilizing fungi include species of *Aspergillus, Fusarium,* and *Penicillium* (Paul and Clark, 1989). A wide variety of heterotrophs solubilize insoluble phosphate including tricalcium phosphate, dicalcium phosphate, hydroxyapatite, and rock phosphate (Altomare, 1999). Bacteria which participate in the reactions include: *Microccocus, Aereobacter, Flavobacterium, Erwinia Pseudomonas, Bacillus, Rhizobium, Burkholderia, Achromobacter* and *Agrobacterium* (Kim *et al.*, 1997,1998). The mechanisms of solubilisation of insoluble phosphate are based on acidification of the medium following organic acid production.

Microbial oxidation of metal sulphides: A wide range of bacteria and fungi have the ability to oxidize metal sulphides, some being chemoautotrophs such as members of the genus *Thiobacillus*, while others are common heterotrophs. The final product of the oxidation reactions involved is sulphate which occurs as sulphuric acid (Killham, 1994). This sulphuric acid can be corrosive to metals, but on the positive side, can be used in ore leaching to obtain metals.

The biogeochemical processes mentioned above and studied here have generally been associated with chemolithotrophic bacteria and the potential role of

heterotrophs in their mediation has generally been underestimated, but are increasingly being shown to play a crucial role in environmental cycling (Killham, 1994). Heterotrophic nitrification and S-oxidation may not benefit organisms in relation to direct end product formation, but through the indirect benefits gained by a heterotroph from participating in these processes. The production of polythionates during S-oxidation by fungi, for example, may help protect these organisms from the toxic effects of heavy metals and other toxicants.

6.2 Materials and Methods

Growth of bacteria and analysis of ions

The bacteria were grown on nutrient agar plates and inoculated into 10 ml of Nutrient Broth containing 0.1% w/v substrate in sterile Falcon Tubes (100ml); the tops were loosened to allow for gas exchange and then incubated with vigorous shaking for 7 days at 37^0C. The contents were then allowed to settle and an aliquot was transferred to a HP-1050 DAD HPLC SYSTEM for analysis of resultant ions, or dipped with the relevant ion dipstick (Figure 6.1).

A B

Figure 6.1: (A). Dipsticks container with dipsticks used for ion determination showing concentration chart, (B), Dipsticks used for ion determination showing concentration chart set used for determination of phosphate.

6.3 Results and Discussion

A comment on Dipsticks as a method for ion analysis. The measurement of ions (which are important in environmental transformations) in this laboratory (such as nitrate, phosphate and sulphate) has generally involved the use of colorimetry. These approaches have worked extremely well and, as result have proved to be very useful; of late however, it has been turned to the use of analytical-ion Dipsticks which are less expensive and are generally less- influenced by interference. They also do not involve the preparation and use of dangerous chemicals (for example when they are used to replace corrosive chromotropic acid in the analysis of nitrate) and can be used to rapidly screen a wide number of

samples. This replacement of chromotrophic acid with Nitrate-Dipsticks provides a good example of the advantages in changing this analytical approach. This analytical reagent is based on concentrated sulphuric acid (Simms and Jackson,1971) and is therefore highly corrosive and is dangerous to prepare and use. Its use as an analytical reagent is also hindered by the fact that, as well as nitrate, it reacts with sugars, when these are present to give a pink-purple colour which interferes with the reading of the normal yellow colour produced by the interaction of chromotropic acid with the nitrate ion. Because no acids are used when nitrate-ion Dipsticks are used, and because no colour interference occurs using this approach, being quicker and cheaper in the long run, is regarded as an improvement on the use of chromotropic acid.

The only disadvantage with using Dipsticks is that some accuracy is sacrificed. In most cases, however, all that is needed from a nitrate ion analysis is a rapid indication of whether or not the ion in question is present or a relatively accurate estimate of its concentration, both of which can be provided using Dipsticks. Tests, by others in this laboratory have shown that results from Dipsticks are between 5 percent (plus or minus) of the values achieve using colorimetry, as was previously used.

The results show that all of the bacteria hydrolysed urea to ammonium and were able to oxidize ammonium to nitrate, via nitrite (Table 6.1). The most active urea hydrolyzer was isolate 7, followed by 5 and 4, while isolate 10 showed the least activity in this respect (Table 6.1). All isolates also oxidized ammonium to nitrate

with the formation of small amounts of nitrite as intermediates. Since the oxidation of nitrite to nitrate is rapid, the former ion rarely appears at high concentration in the environment (Killham, 1994). In terms of nitrate production, bacterium 7 was the most active, followed by 10 and 5, while bacteria 1 and 2 were the least active (Table 6.2).

Table 6.1. Hydrolysis of urea to ammonium.

Substrate-Urea	Ammonium ($\mu g ml^{-1}$)	
	1	27.5 (1.9) **30**
	2	25.3 (2.7) **15**
	3	26.7 (0.9) **25**
	4	30.6 (3.6) **30**
	5	43.6 (5.2) **50**
	6	13.1 (2.1) **15**
	7	50.9 (2.3) **60**
	8	10.8 (8.6) **5**
	9	17.3 (1.9) **20**
	10	4.4 (0.2) **10**

1) *Bacillus licheniformis*, 2) *Bacillus subtilis*, 3) *Bacillus thuringiensis*
4) *Enterococcus mundtii*, 5) *Citrobacter freundii*, 6) *Pseudomonas luteola*
7) *Arthrobacter sanguinis*, 8) *Klebsiella oxytoca*, 9) *Kocuria rhizophila*, 10) *Rothia amarae*.

Figures in **bold** relate to Dipstick analysis. Means of triplicate flasks (+/- standard deviation), 7day incubation at 37°C, values in excess of control value.

Table 6.2. Oxidation of ammonium to nitrite and nitrate.

Substrate-Urea	Product (µg ml^{-1})
Nitrite	Nitrate
1. 1.8. (1.9) **All- trace**	5.2 (0.66) **8**
2. 0.7 (0.1)	3.2 (0.8) **Trace**
3. 0.9 (0.9)	11.9 (1.2) **10**
4. 1.4 (0.60)	15.9 (2.0) **20**
5. 0.3 (0.0.2)	30.2 (0.9) **25**
6. 1.1 (0.1)	10.2 (0.1) **15**
7. 0.5 (0.2)	50.3 (07) **35**
8. 0 (0.1)	7.9 (1.3) **10**
9. 1.9 (0.1)	20.9 (1.7) **20**
10. 1.4 (0.2)	30.2 (5.4) **50**

1) *Bacillus licheniformis*, 2) *Bacillus subtilis*, 3) *Bacillus thuringiensis*
4) *Enterococcus mundtii*, 5) *Citrobacter freundii*, 6) *Pseudomonas luteola*
7) *Arthrobacter sanguinis*, 8) *Klebsiella oxytoca*, 9) *Kocuria rhizophila*, 10) *Rothia amarae.*

Figures in **bold** relate to Dipstick analysis. Means of triplicate flasks (+/- standard deviation), 7day incubation at 37 ^{0}C, values in excess of control value.

All of the isolates were able to solubilize insoluble phosphate, notably isolate 7 followed by isolate 5, with isolate 10 being the least effective. Similarly, all isolates were able to oxidize iron sulphide to release Fe^{2+} and oxidize copper to sulphide to release Cu^{2}+ ions. All of the isolates, with the exception of isolate 2,

released similar amounts of Fe^{2+}, while isolate7 and 5 were particularly active at oxidizing copper sulphide (Table 6.3).

Table 6.3. Solubilization of insoluble P and oxidation of FeS and CuS.

Substrate-		Product (µg ml^{-1})	
Insoluble-P to Phosphate		FeS to Fe^{2}+	CuS to Cu^{2}+
1	26.5 (1.3**)** **30**	3.1 (0.9**) All- trace**	4.2 (1.6) **4**
2	5.3 (2.7) **15**	1.7 (0.2)	3.6 (1.8) **4**
3	4.7 (1.9) **20**	4.9 (1.9)	5.9 (1.2**)** **7**
4	25.6 (4.6) **30**	4.4 (1.6)	14.6 (1.8) **10**
5	45.6 (4.2) **40**	3.0 (1.2)	23.2 (1.9) **20**
6	18.1 (1.1) **10**	5. 0 (0.5)	10.4 (1.1) **10**
7	45.9 (1.3) **50**	3.5 (0.2)	25.3 (2.7) **15**
8	20.8 (8.5) **15**	4.0 (0.9)	17.9 (1.5) **20**
9	15.3 (1.6) **15**	5.0 (0.2)	12.9 (1.7) **10**
10	6.4 (1.2) **5**	2.4 (2.2)	12.2 (1.4) **30**

1) *Bacillus licheniformis*, 2) *Bacillus subtilis*, 3) *Bacillus thuringiensis*
4) *Enterococcus mundtii*, 5) *Citrobacter freundii*, 6) *Pseudomonas luteola*
7) *Arthrobacter sanguinis*, 8) *Klebsiella oxytoca*, 9) *Kocuria rhizophila*, 10) *Rothia amarae.*

Figures in **bold** relate to dipstick analysis. Means of triplicate flasks (+/- standard deviation), 7day incubation at 37°C, values in excess of control value.

The results obtained using proprietary Dipsticks were in most cases similar enough to this obtained using HPLC to point to their use in experiment where an exact, but reasonably close figure for an ion-concentration is required. As mentioned above, this loss of accuracy is acceptable for convenience, low cost and safety of using Dipsticks instead of the colorimetric assay. The results show that the bacteria isolated from healthcare environments are capable of participating in some important metabolic process, whether such participation is relevant to such environments, especially where carbon is limiting, is not immediately clear. Despite this, the experience of conducting these experiments was, in any case, highly valuable.

CHAPTER 7

FINAL DISCUSSION

The work provided in this Thesis clearly shows that bacteria and other microbes commonly contaminate everyday objects and surfaces, a fact which does not generally cause problems in normal life (except for the occasional food poisoning episode). Such contamination does, of course, have major implications in health care settings such as hospitals and in particular for immunocompromised patients. These patients have their immune systems inhibited either intestinally (e.g. during organ transplantation), or as the result of a natural intervention, such as AIDS. The microbes which cause these infections are often generally not pathogenic and the immune systems of non–immunocompromised patients can generally cope with them, even when the patient is otherwise ill. The stark fact is that any microbe can act as pathogen in people with a compromised immune system. It is therefore extremely important to make certain that all surfaces in health care settings are as clean and microbe-free as possible and that this hygiene status includes non-pathogens as well as the generally recognized pathogens. Such a relatively microbe-free environment can be achieved using biocides, but there is no substitute for thorough “deep cleaning”.

The cleaning of hospital surfaces is the main defence against the threat of antibiotic resistant bacteria and nosocomial infections. While the importance of deep cleaning is universally recognized, this does not mean that such cleaning programmes are theoretically effective or always well-managed. Bleach is by far the most commonly used biocide in both hospital and domestic settings and, when used correctly, can be

extremely efficient and act as an effective standby for all disinfecting purposes. Although it is more expensive, hydrogen peroxide provides a useful alternative to bleach especially for use on so-called “non-critical surfaces” since it is fact acting and exhibits a broad spectrum antimicrobial activity against bacterial and fungal spores and viruses; steam vapour systems and microfiber- containing biocides can also be effectively employed for routine cleaning purposes.

An essential requirement for successful disinfection is the provision of an adequate contact time between a disinfectant and the object being disinfected. Such contact times vary in addition to a number of environmental factors, notably the degree of microbial loading. Pathogens, and other microbes, can be transmitted in a number of ways in the hospital environment, including:

Droplet contact transmission: A large number of diseases are spread inside droplets which make contact with the eye, nose or mouth. Examples of these droplet infections include SARS, the common cold, Legionnaires' disease and MRSA.

Such infected droplets are produced by infected persons when coughing, sneezing or talking.

Airborne Transmission: Suspended dust particles which contain microbes often remain in the air over long periods and from here can gain entry into the upper and lower respiratory tracts and thereby bring about infections like Aspergillosis, chickenpox and measles.

Faecal-oral transmission: Pathogenic and non-pathogenic microbes infect patients following the consumption of food and water which has been contaminated with

faeces. Bad hygiene and poor sanitation allow such microbes to contaminate food, water and environmental surfaces. These organisms then multiply inside the digestive system then released from the body in faeces and urine, so that the infection-cycle then begins again. Diseases which are disseminated in this way include: rotavirus, hepatitis A virus, *E. coli*, *Cryptosporidium, C. difficile, H. pylori* and *Candida.*

Direct contact transmission: This disease-transmission process involves the direct physical contact between an infected person and the new host; examples include, kissing and sexual intercourse, or merely close contact. Diseases which are spread by direct contact transmission include H1N1 virus and hepatitis A virus, *Acinetobacter*, *E. coli*, SARS, the common cold, ringworm and other yeast infections, scarlet fever, norovirus, foot and mouth disease, *H. pylori*, and MRSA.

Indirect contact transmission: This process of disease spread takes place when a susceptible person makes direct physical contact with the body surfaces of an infected person via their hands, and then touches their own face, eyes or mouth, allowing the pathogen to gain access into the body and initiate infection. Organisms which use this transmission route include: *rotavirus,* hepatitis A virus, influenza, the common cold, *H. pylori* and tuberculosis, norovirus, *C. difficile,* MRSA, SARS, *E. coli, Cryptosporidium,* ringworm and other yeast infections and scarlet fever. The fact that these microbes can survive and be replenished on body surfaces for long periods demonstrates the obvious need for hand washing and other aspects of body hygiene amongst patients, staff and hospital visitors.

Use of disinfectants and detergents in healthcare settings

The above discussion demonstrates the clear need for effective sterilizing agents to reduce the pathogen load on surfaces in hospitals. The use of such agents varies based upon factors such as efficiency and cleaning ability, environmental impact, cost, and associated toxic effects.

Detergents

Detergents generally need effort in regard to rubbing and scrubbing to be fully effective but are good at removing chemicals, food spills, and other commercial wastes. They are not, however, generally suitable for use in cleaning blood or other body fluids from contaminated surfaces and are also usually not effective against bacterial spores, particularly those of *C. difficile.*

Sterilizing agents

Sterilizing agents are generally expansive and highly toxic and are therefore not used in routine household or day to day use. They are however, effective on so-called "critical surfaces" in hospital, industrial and laboratory settings. These agents are however, very effective at killing pathogens, including spores of *C. difficile*, and are particularly effective for use in disinfecting and removing blood and other contaminating body fluids; they include agents such as chemicals, heat, irradiation, filtration and high pressure sterilization.

Guidelines for use in the decontamination of healthcare associated surfaces

Consideration needs to be given to the sterilization of the numerous surfaces found in health care environments, simply because each site varies in its surface properties and the environmental conditions to which it is exposed. An obvious example is provided by the differing conditions found on the surface of an oven compared to that of a refrigerator.

Non-critical medical surfaces

These areas can be adequately served by routine, low maintenance, detergent-based cleaning which will prevent the transmission of microbes from non-critical surfaces, such as furniture and floors. The cleaning process should begin the removal of soil and other debris by wiping or deep scrubbing before a cleaning/disinfecting agent is applied. The survival of bacteria such as *Staphylococcus* spp., MRSA, *Acinetobacter*, and other airborne fungi is encouraged by the presence of dust on surfaces and damp-dusting with cloths wetted with detergents recommended for use on such non-critical surfaces, followed by a period thorough drying. All objects within the ward or room including radiators, air conditioning units, fans, switches, sockets and of course computer areas should be thoroughly wiped with disinfectant-rich cloths. Doors, which include their edges, should be cleaned and special attention should be given to areas which are frequently touched such as handles and door-push plates. In order to control Legionnaires' disease, any infrequently used taps and shower heads should be run weekly for around 10 minutes and all air conditioning and ventilation grills and

associated extractors and inlets should be dusted at least weekly and should be fully cleaned on a yearly basis. Walls and ceilings however, need to be washed only every 6 months or so, by the use of hot water and detergent.

The following factors affect the choice and use of disinfectants. Attention should always be given to the most important factor in their use, namely contact–exposure time:

- The need to comply with the appropriate chemical safety regulations.
- Some disinfectants corrode or discolour surfaces, so compatibility should be considered and compatibility tests conducted.
- The required antimicrobial activity- this relates to the need to determine if the proposed has a wide antimicrobial spectrum?
- Contact times- the necessary contact time needed to kill nearly are hundred percent of the pathogens present needs to be determined by laboratory tests.
- Is the disinfecting agent effective when organic matter is present? This is a very important point because organic matter rapidly deactivates many otherwise potent disinfecting agents?
- Storage and disposal -Is the agent stable when stored for long periods? This is an important point because such agents are often bought in bulk to reduce costs and are stored for long periods; storage should of course be done at room temperature in the dark. Issues regarding the disposal of an agent and its environmental toxicity obviously need to be considered; some healthcare authorities may wish to impose ethical environmental tests on the sterilizing products they employ.

- Environmental factors- Do common environmental factors such as temperature and pH affect the disinfectant's effectiveness?
- Costs-Finally, cost is an essential factor especially since healthcare facilities world-wide are increasingly being effected by Government cost-cutting.

Disinfectants used in routine cleaning of healthcare environments

The following is a description of the most frequently used, EPA-registered disinfectants:

- Phenolic and iodophore-based germicides.
- Quaternary ammonium germicidal detergents.
- Hydrogen peroxide (3-7.5%).
- Ethyl or isopropyl alcohol (70-90%); sodium hypochlorite, i.e. bleach (5.25-6.15% household bleach diluted 1:500 gives >100 ppm available chlorine).

Environmentally safe disinfectants

So-called environmentally safe disinfectants include baking soda, vinegar, eucalyptus oil, grapefruit seed extract borax, liquid detergent, alcohol and tea tree oil. With the exception of undiluted vinegar and eucalyptus oil, most of these disinfectants do not kill *E. coli.*

Antibacterial coating of surfaces

Antimicrobial coatings are available for use on commonly used domestic fabrics, including, linen (curtains); furniture (chairs and tables); office equipment (computers and printers); hand-touch sites (handles and water taps) and generally used surfaces such as walls, floors, walls and doors. Any product that can be impregnated or coated with a micro-biocidal paint or chemical can referred to as being ‘antibacterial’. Such bioactive surfaces or coatings generally provide heavy metals, antiseptics and biocide to the surface undergoing treatment. Nano-silver particles, like titanium dioxide, are particularly useful since they form an invisible protective nano-coating which can act as a very effective biocide for use on a wide range of surfaces, even under extreme temperatures.

CONCLUSIONS

A wide range of bacteria were isolated during the course of this study from computer keyboards, sinks, used toothbrushes and vacuum cleaner dust. Bacteria were also shown to be emitted by toilet hand dryers; these are becoming increasingly popular in public buildings because of reasons of cost and convenience. The results of work presented here shows, however, that paper towels should be used in healthcare environments instead of these dryers, simply because hand dryers can release potential pathogens into the surrounding air, into what is often a small, enclosed space, with little in the way of ventilation. Studies are also reported on the survivability of bacteria on smooth and rough tiles, essentially the same similar to those found in homes and

healthcare settings. Seemingly paradoxically, bacteria were shown to survive for longer on rough, compared to smooth tiles as well as on plastic plumbing fittings than on copper fittings. These findings confirm those of other works, by showing that copper fittings are desirable over plastic fittings because they dramatically reduce the survival of surface-growing, potential pathogens. The results presented here also show that bacteria are important nosocomial pathogens and, since they have been shown to be widely isolatable from the hospital and other indoor environments studied here, they will likely cause life-altering diseases in hospital specially for immunocompromised patients. Clearly the existence and survival in healthcare settings of these potentially pathogenic bacteria is a highly important research area which deserves continued investigation.

SUGGESTIONS FOR FURTHER STUDIES

The following important areas of research which have been examined in this Thesis need to be further studied: a) the survival of potentially pathogenic bacteria on tiles, b) the ways in which potentially pathogenic bacteria can survive on different types of piping used in plumbing in hospitals and c) the part played by hand dryers in distributing bacteria and other microbes inside the environment of hospitals and other healthcare facilities.

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APPENDIX 1

Publications Arising From This Thesis

Bacterial contamination of used manual toothbrushes and effects of toothpastes on isolated potential pathogens

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Toothbrushes play an essential role in oral hygiene and are commonly found in community and hospital settings. The toothbrushes may act as a reservoir for potential pathogens transferred from the oral cavity and from the bathroom environment. The purpose of this study is to determine the bacterial contamination of used toothbrushes and determine the antibacterial effect of toothpastes. Scanning electron microscopy (SEM) was used to visualize biofilms on toothbrush bristles. 50 used toothbrushes obtained from volunteers were analysed bacteriologically using standard microbiological techniques. Bacteria present on all toothbrushes heads were cultured to determine the presence of bacteria and scanned by SEM. The antibacterial effect of toothpastes was determined using seven types of commercial toothpastes and chlorhexidine toothpaste by inoculation bacteria on the toothpaste plates. The result showed that all the toothbrushes were contaminated with the following bacteria: *Roseomonas mucosa, Stenotrophomonas maltophilia, Pseudomonas aeruginosa, Leclercia adecarboxylata, Enterobacter asburiae, Candidatus Roseomonas massiliae, Pseudomonas parafulva, Bacillus licheniformis, Pseudomonas aeruginosa, Agrobacterium larrymoorei, Pantoea septica, Stenotrophomomnas rhizophila, Citrobacter freundii* and *Pseudomonas frederiksbergensis*. The bristle surfaces, being rough, provided ample sites for trapping organisms. Examination of a brush revealed a biofilm on the brush head. The biofilm seen on the surface of the head to be composed of a compacted mixed community of microorganisms, including cocci, bacilli and filamentous organisms, together with cellular and debris. The toothpaste used proved antibacterial and inhibited bacterial growth, based mainly in the activity of fluoride which is widely used as an effective anticaries agent. In conclusion the isolated organisms are potentially pathogenic, particularly in relation to immunocompromised patients. The appropriate rinsing and drying of the toothbrushes before storage will however, likely reduce the incidence of these bacteria and the health risk associated with these pathogens.

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7th World Congress on Microbiology, November 28-29, 2016 Valencia, Spain

Influence of copper and plastic surfaces on the survival of bacteria in relation to the health care environment

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University of Sheffield, UK

Metallic copper (Cu) surfaces have antimicrobial properties against a variety of different microorganisms and copper touch surfaces are likely to be increasingly used in public places including hospitals. Studies in the literature show that molecular mechanisms result in the rapid killing of Cu surface-exposed bacteria and yeasts result from a sharp shock of extreme and immediate Cu-ion overload combined with severe membrane and cell envelope damage, although similar low mutation rates have been observed in cells obtained from both Cu and control surfaces. The aim of this study was to determine the survival of bacteria on the surfaces of copper and plastic plumbing surfaces. The antibacterial activity of copper surfaces was determined by overlying suspensions of Staphylococcus aureus and Escherichia coli on copper and plastic surfaces. All pipes were sterilized and bacterial suspensions from colonies were prepared and then the pipes were contaminated by the bacterial suspension. The experiments were performed at 18-23°C and the results were assessed after a 20-day exposure. The numbers of viable bacteria in the suspension were determined by serial dilution and plating on Nutrient Agar plates; the plates being incubated at 37°C for 48 h. The results showed that low counts of Staphylococcus aureus were seen on copper surfaces, as compared with those obtained on the plastic, control surfaces, i.e., the results show that E. coli failed to survive on copper pipes. The number of bacteria isolated from the plastic surfaces was consistently higher than the number isolated from copper surfaces. The survival rate of bacteria on the copper surfaces was low and none of the inoculated bacteria survived after 20 days of exposure. Copper is well known to be an antibacterial, and its use in medical environments is likely to the lead to the continuous reduction of environmental microbial contamination, including MRSA. The studies presented here show that the incorporation of Cu in healthcare facilities may dramatically help reduce the environmental microbial burden and act as a useful adjunct to current infection prevention and control systems, despite the fact that bacteria will eventually acquire resistance to the ion.

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8th CLINICAL MICROBIOLOGY CONFERENCE October 26-28, 2017 | Paris, France

Factors Influencing the Survival of Pathogenic Microbes in the Built (i.e. hospitals) and Natural Environments

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Abstract

Bacteria and yeast can survive for 3 days on ceramic tiles.
Toilet air hand dryers can spread bacteria around the room and on the hands of the user.
The number of hand-contaminating bacteria from the hand dryer increases with time of use

Introduction

The hospital environment is a potential reservoir of bacterial pathogens living in associated with patients with diverse pathogenic microorganisms and a large number of susceptible individuals linked to significant morbidity and mortality. Bacterial pathogens have an innate ability to survive on surfaces in the hospital environment, often for long periods of time (1). Bacterial pathogens isolated from hospital environment are continuing to develop resistance to multiple antimicrobial agents. The emergence of multi-drug resistant organisms in hospital causes major problems in the treatment of nosocomial infections. The environment of patients is heavily contaminated by infectious multidrug resistant organisms, including methicillin-resistant *S. aureus* (MRSA), vancomycin-resistant enterococci (VRE), *Clostridium difficile, Acinetobacter baumannii* and *Pseudomonas aeruginosa* are an emerging, which caused well-known problem in healthcare systems (3).

Aims of the project

The aim of the work done in this study was a) to determine the occurrence of various bacteria and fungi on surfaces in the built environment, b) to determine the survival rates of these organisms on such surface environments, and c) determine factors that influence such survival.

Methods

1- Determine the survival rates of *Staphylococcus auerus* and *Escherichia coli* on types of sterilized ceramic tiles . The number of bacteria was determined from 3rd day, then 5, 15, and 20 days(2).

2- Assessment of the number of microorganisms on hands after washing and drying by warm air hand dryers, Then hands were touch the surface of nutrient agar plate and incubated at 37°C for 48 h and scored for the presence or absence of growing bacteria

3- Quantification of bacteria transferred from hand warm air dryers. The bacteria were counted and measured the effect of drying times (4).

Results

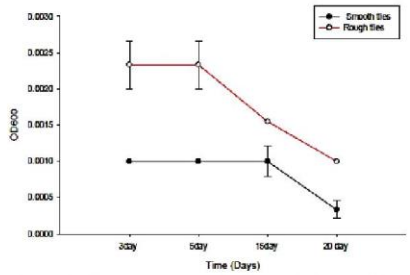

Figure 1: Survival of *S. aureus* on ceramic tiles under dry conditions

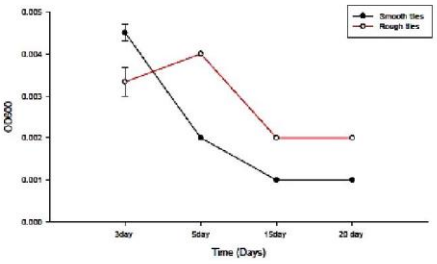

Figure 2: Survival of *E. coli* on ceramic tiles under dry conditions

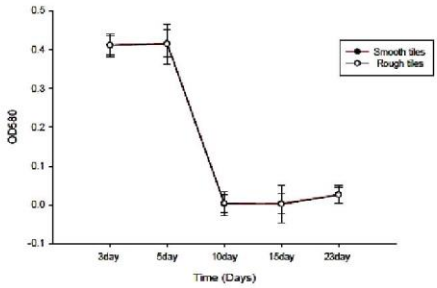

Figure 3: Survival of *Candida rugosa* on ceramic tiles under dry conditions

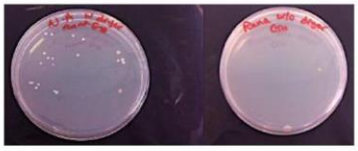

Figure 4: Agar plates used to assess the occurrence of bacteria on hands. (Left) hand washed and dried with a warm air dryer, (Right) hand washed and dried without a warm air dryer.

	WAD1	WAD2	WAD3
5 Sec	0	12	19
10 Sec	2	17	20
15 Sec	5	18	15
20 Sec	6	22	24
25 Sec	3	18	10
30 Sec	9	16	8
35 Sec	12	50	11
40 Sec	10	37	20
45 Sec	23	15	18
50 Sec	41	49	30
55 Sec	31	44	21
60 Sec	30	63	19

Table 1: The mean bacterial count using three different types warm air dryer (WAD) for different drying times.

Conclusion

To conclude, these environmental surfaces have been shown to carry both non-pathogenic and pathogenic bacteria. Therefore, a single hand contact with a contaminated surface could result in a variable degree of pathogen transfer. In this age of increasing antibiotic resistance, these survival data indicate that the appropriate disinfection of the environment and control procedures should be used to control of infections in hospitals.

Future work

- In the future, I will continue to isolate bacteria and *Candida* from environmental surface.
- Determine their survival rates and also the factors which influence this survival.
- I will also determine if antibiotic resistant bacteria are better able to survive than non-resistant types

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Bacterial Contamination of Used Manual Toothbrushes and Effects of Toothpastes on Isolated Potential Pathogens

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Abstract

All the toothbrushes were contaminated with bacteria.
Toothpastes which contains fluoride or chlorhexidine acts as an antibacterial and inhibits bacterial growth.
The biofilm on the brush head to be composed of a compacted mixed community of microorganisms, including cocci, bacilli and filamentous organisms, together with cellular and other debris.

Introduction

Toothbrushes play an essential role in oral hygiene and are commonly found in community and hospital settings. The toothbrushes may act as a reservoir for potential pathogens transferred from the oral cavity, the bathroom environment, from storage containers and the water used for rinsing and the users. Contaminated toothbrushes have been suggested to play a role in both systemic and localized diseases. The possibility of toothbrushes being associated with the transmission of heart diseases, arthritis, bacteremia and stroke have also been reported.

Aims of the project

The aim of the work done in this study was to a) isolate, characterize and identify the bacterial contaminants on used manual toothbrushes. b) determine the antibacterial effect of toothpastes. C) Scanning electron microscopy (SEM) was used to visualise biofilms on toothbrush bristles.

Methods

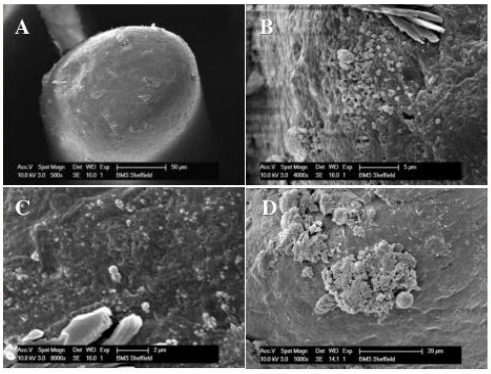
1- Fifty used toothbrushes obtained from students and volunteers were analysed bacteriologically using standard microbiological techniques.
2- Scanning toothbrushes heads using SEM by immersing them in 2.5% glutaraldehyde in 0.1M sodium cacodylate buffer, pH7.3, for 60min. Brushes was rinsed, dehydrated in ethanol and dried from liquid CO2. examined using a JEOL JSM-5300lv scanning electron microscope at an accelerating voltage of 10–30 kV.
3- Determination the antibacterial effect of toothpastes using seven types of commercial toothpastes and chlorhexidine toothpaste by inoculation *Staphylococcus aureus* and *Escherichia coli* on the toothpaste plates.

Results

Table (1): Bacterial Isolates from the Used Manual Toothbrushes

Roseomonas mucosa
Stenotrophomonas maltophilia
Leclercia adecarboxylata
Enterobacter asburiae
Candidatus Roseomonas massiliae
Pseudomonas parafulva
Bacillus licheniformis
Pseudomonas aeruginosa
Agrobacterium larrymoorei
Pantoea septica
Stenotrophomomnas rhizophila
Citrobacter freundii
Pseudomonas frederiksbergensis

Figure (1): Scanning electron microscopy of toothbrush biofilms on manual toothbrushes used for approximately 3 months. A) showing debris and cocci bacteria; B) showing debris and biofilm;) image of tip of bristle, showing indentations and crevasses; down right) cocci embedded in the biofilm.



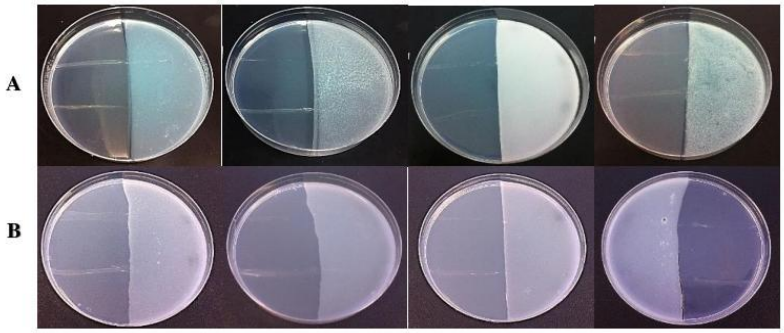


Figure (2) : A) commercial toothpastes agar plates that inoculated by *Staphylococcus aureus* and *Escherichia coli* and B) chlorhexidine toothpaste agar plates that inoculated by the same bacterial strains.

Conclusion

To conclude, the isolated organisms are potentially pathogenic, particularly in relation to immunocompromised patients. The appropriate rinsing and drying of the toothbrushes before storage will however, likely reduce the incidence of these bacteria and the health risk associated with these pathogens.

Future work

- In the future, I will continue to isolate bacteria and *Candida* from environmental surface.
- Determine their survival rates and also the factors which influence this survival.
- I will also determine if antibiotic resistant bacteria are better able to survive than non-resistant types.

References

1- Frazelle, M.R. and Munro, C.L. (2012). Toothbrush contamination: a review of the literature. *Nursing Research and Practice*. Vol. 2012
2- Samuel, O. and Ifeanyi, O. (2015). Bacterial Contamination of Used Manual Toothbrushes Obtained from Some Students of Nnamdi Azikiwe University Awka, Nigeria. *Universal Journal of Microbiology Research* 3(4): 56-59
3- De Rossi, A., Ferreira, D., da Silva, R., de Queiroz, A., da Silva, L., Nelson-Filho, P. (2014). Antimicrobial Activity of Toothpastes Containing Natural Extracts, Chlorhexidine or Triclosan. *Brazilian Dental Journal* 25(3): 186-190
4- Marquis, R.E. (1995). Antimicrobial actions of fluoride for oral bacteria. *Canadian Journal of Microbiology*. 41: 955-964
5- Munir, A., Umar, J., Hameed, A. and Ahmed, S. (2005). The effect of commercially available local brand of toothpastes against oral bacteria. *Pakistan Oral and Dental Journal*. 25 (1):35-40

APPINDIX 2

The phylogenetic analysis of bacteria isolated from environment samples

1- The phylogenetic analysis of bacteria isolated from sink samples

Klebsiella oxytoca CP011618.1

Klebsiella oxytoca strain CAV1335, complete genome

Sequence ID: gb|CP011618.1| **Length:** 6229565 **Number of Matches:** 8

Range 1: 2928343 to 2929103 GenBank Graphics ▼ Next Match ▲ Previous Match

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Features: SAM-dependent methyltransferase
rRNA-16S ribosomal RNA

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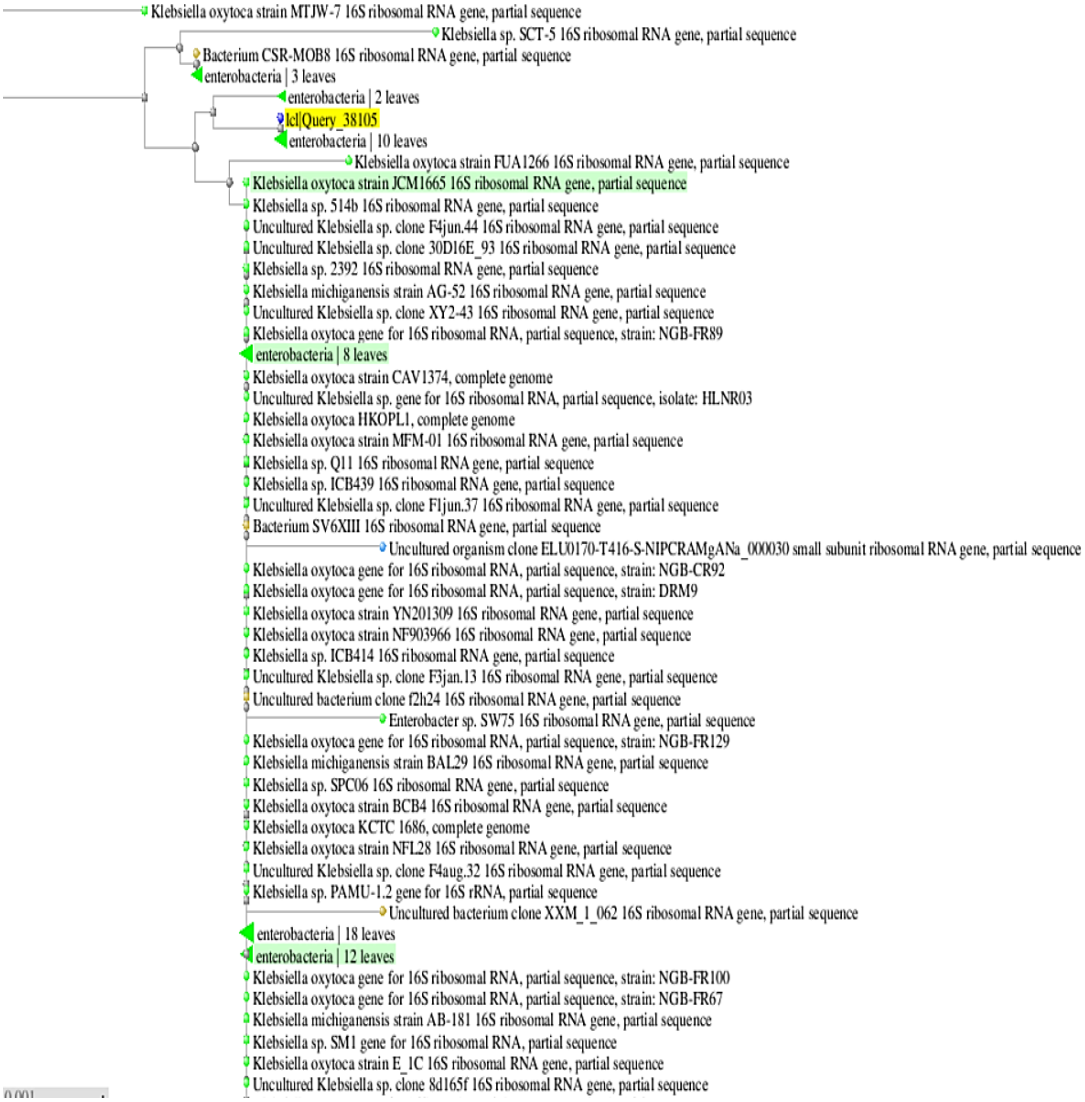
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enterobacteria | 2 leaves
lcl|Query_38105
enterobacteria | 10 leaves
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Klebsiella oxytoca strain JCM1665 16S ribosomal RNA gene, partial sequence
Klebsiella sp. 514b 16S ribosomal RNA gene, partial sequence
Uncultured Klebsiella sp. clone F4jun.44 16S ribosomal RNA gene, partial sequence
Uncultured Klebsiella sp. clone 30D16E_93 16S ribosomal RNA gene, partial sequence
Klebsiella sp. 2392 16S ribosomal RNA gene, partial sequence
Klebsiella michiganensis strain AG-52 16S ribosomal RNA gene, partial sequence
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Klebsiella oxytoca gene for 16S ribosomal RNA, partial sequence, strain: NGB-FR89
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Klebsiella oxytoca strain CAV1374, complete genome
Uncultured Klebsiella sp. gene for 16S ribosomal RNA, partial sequence, isolate: HLNR03
Klebsiella oxytoca HKOPL1, complete genome
Klebsiella oxytoca strain MFM-01 16S ribosomal RNA gene, partial sequence
Klebsiella sp. Q11 16S ribosomal RNA gene, partial sequence
Klebsiella sp. ICB439 16S ribosomal RNA gene, partial sequence
Uncultured Klebsiella sp. clone F1jun.37 16S ribosomal RNA gene, partial sequence
Bacterium SV6XIII 16S ribosomal RNA gene, partial sequence
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Enterobacter sp. SW75 16S ribosomal RNA gene, partial sequence
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Klebsiella michiganensis strain BAL29 16S ribosomal RNA gene, partial sequence
Klebsiella sp. SPC06 16S ribosomal RNA gene, partial sequence
Klebsiella oxytoca strain BCB4 16S ribosomal RNA gene, partial sequence
Klebsiella oxytoca KCTC 1686, complete genome
Klebsiella oxytoca strain NFL28 16S ribosomal RNA gene, partial sequence
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enterobacteria | 12 leaves
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Klebsiella oxytoca gene for 16S ribosomal RNA, partial sequence, strain: NGB-FR67
Klebsiella michiganensis strain AB-181 16S ribosomal RNA gene, partial sequence
Klebsiella sp. SM1 gene for 16S ribosomal RNA, partial sequence
Klebsiella oxytoca strain E_1C 16S ribosomal RNA gene, partial sequence
Uncultured Klebsiella sp. clone 8d165f 16S ribosomal RNA gene, partial sequence

Bacillus subtilis KP340123.1

Bacillus subtilis strain W6 16S ribosomal RNA gene, partial sequence

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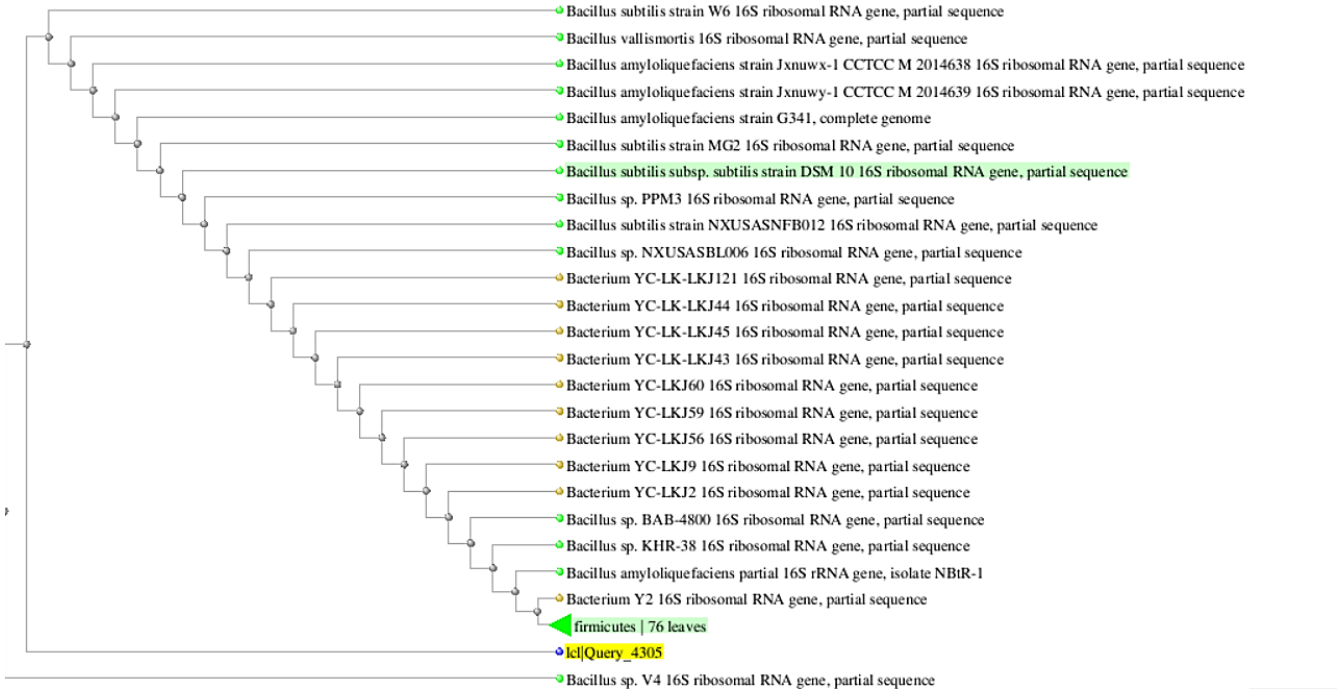
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Bacillus amyloliquefaciens strain Jxnuwy-1 CCTCC M 2014639 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain G341, complete genome
Bacillus subtilis strain MG2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence
Bacillus sp. PPM3 16S ribosomal RNA gene, partial sequence
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Bacterium YC-LKJ9 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ2 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4800 16S ribosomal RNA gene, partial sequence
Bacillus sp. KHR-38 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens partial 16S rRNA gene, isolate NBtR-1
Bacterium Y2 16S ribosomal RNA gene, partial sequence
firmicutes | 76 leaves
lcl|Query_4305
Bacillus sp. V4 16S ribosomal RNA gene, partial sequence

Kocuria rhizophila KM978822.1

Kocuria rhizophila strain AHT-1 16S ribosomal RNA gene, partial sequence

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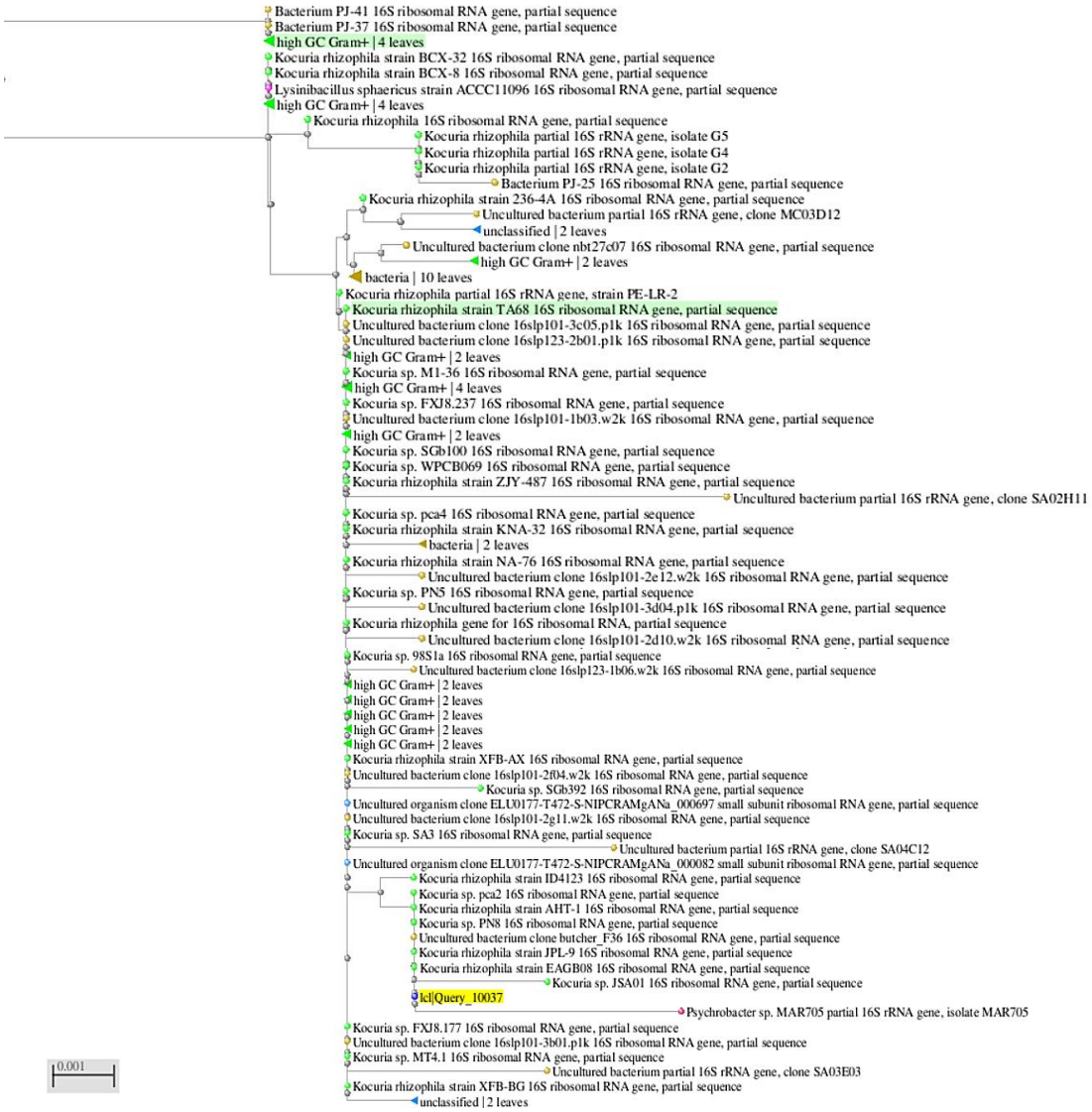
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Bacterium PJ-37 16S ribosomal RNA gene, partial sequence
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Kocuria rhizophila strain BCX-8 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain ACCC11096 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 4 leaves
Kocuria rhizophila 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila partial 16S rRNA gene, isolate G5
Kocuria rhizophila partial 16S rRNA gene, isolate G4
Kocuria rhizophila partial 16S rRNA gene, isolate G2
Bacterium PJ-25 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain 236-4A 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone MC03D12
unclassified | 2 leaves
Uncultured bacterium clone nbt27c07 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
bacteria | 10 leaves
Kocuria rhizophila partial 16S rRNA gene, strain PE-LR-2
Kocuria rhizophila strain TA68 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-3c05.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-2b01.p1k 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
Kocuria sp. M1-36 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 4 leaves
Kocuria sp. FXJ8.237 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-1b03.w2k 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
Kocuria sp. SGb100 16S ribosomal RNA gene, partial sequence
Kocuria sp. WPCB069 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain ZJY-487 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SA02H11
Kocuria sp. pca4 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain KNA-32 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Kocuria rhizophila strain NA-76 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-2e12.w2k 16S ribosomal RNA gene, partial sequence
Kocuria sp. PN5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-3d04.p1k 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila gene for 16S ribosomal RNA, partial sequence
Uncultured bacterium clone 16slp101-2d10.w2k 16S ribosomal RNA gene, partial sequence
Kocuria sp. 98S1a 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-1b06.w2k 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
high GC Gram+ | 2 leaves
high GC Gram+ | 2 leaves
high GC Gram+ | 2 leaves
high GC Gram+ | 2 leaves
Kocuria rhizophila strain XFB-AX 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-2f04.w2k 16S ribosomal RNA gene, partial sequence
Kocuria sp. SGb392 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0177-T472-S-NIPCRAMgANa_000697 small subunit ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-2g11.w2k 16S ribosomal RNA gene, partial sequence
Kocuria sp. SA3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SA04C12
Uncultured organism clone ELU0177-T472-S-NIPCRAMgANa_000082 small subunit ribosomal RNA gene, partial sequence
Kocuria rhizophila strain ID4123 16S ribosomal RNA gene, partial sequence
Kocuria sp. pca2 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain AHT-1 16S ribosomal RNA gene, partial sequence
Kocuria sp. PN8 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone butcher_F36 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain JPL-9 16S ribosomal RNA gene, partial sequence
Kocuria rhizophila strain EAGB08 16S ribosomal RNA gene, partial sequence
Kocuria sp. JSA01 16S ribosomal RNA gene, partial sequence
lcl|Query_10037
Psychrobacter sp. MAR705 partial 16S rRNA gene, isolate MAR705
Kocuria sp. FXJ8.177 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp101-3b01.p1k 16S ribosomal RNA gene, partial sequence
Kocuria sp. MT4.1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SA03E03
Kocuria rhizophila strain XFB-BG 16S ribosomal RNA gene, partial sequence
unclassified | 2 leaves
0.001

Bacillus cereus KC731425.1

Bacillus cereus strain VITSH1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KC731425.1| **Length:** 1369 **Number of Matches:** 1

Range 1: 513 to 1353 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1283 bits(1422)	0.0	789/841(94%)	0/841(0%)	Plus/Minus

```
Query  1     ACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGATTAC  60
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1353  ACGGGCGGGGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGATTAC  1294

Query  61    TAGCGATTCCAGCTTCATGTATGCAAGTTGCAACCGACAATCCAAACTGAAAACGGTTTT  120
             |||||||||||||||| ||| |||||||||| || ||||||||||||||||||||||||||
Sbjct  1293  TAGCGATTCCAGCTTCAGGTAGGCAAGTTGCAGCCTACAATCCAAACTGAAAACGGTTTT  1234

Query  121   ATGATATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCATTGTAACACGTGT  180
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1233  ATGAAATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCATTGTAGCACGTGT  1174

Query  181   GTACCCCAGGTCATAGGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGT  240
             ||| |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1173  GTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGT  1114

Query  241   CACCGGCAGTCACCTTAAAGTGCCCAACTTATGGATGGCAAGTAAGATCAAGGGTTGCGC  300
             |||||||||||||||||||||||||||||| |  |||||||| ||| ||||||||||||||
Sbjct  1113  CACCGGCAGTCACCTTAAAGTGCCCAACTAAATGATGGCAACTAAAATCAAGGGTTGCGC  1054

Query  301   TCGTTGCGGGACTTAACCCAACATCTCACAACACAACCTGACAACAACCATGCACCACCT  360
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  1053  TCGTTGCGGGACTTAACCCAACATCTCACAACACAAGCTGACAACAACCATGCACCACCT  994

Query  361   GTCACTCTGCTCCCGAAGGAAAAGACCTATCTCTAGGGTTTTCACAGGATGTCAAGAGCT  420
             |||||||||||||||||||||||| |||||||||||||| ||| |||||||||||| ||
Sbjct  993   GTCACTCTGCTCCCGAAGGAAAAGCCCTATCTCTAGGGTTGTCAAAGGATGTCAAGACCT  934

Query  421   GGTAAGGGTCTTCCCGTTGCTTCCAATTAAACCACATGCTCCACCGCTTGGGCGGGCCCC  480
             ||||||| ||||| ||||||||| ||||||||||||||||||||||||| |||||||||
Sbjct  933   GGTAAGGTTCTTCGCGTTGCTTCAAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCC  874

Query  481   CGTCAATTCCTTTGAATTTCAACCTTGCGGACGTACTCCCCAGGGGGAATGGTTAATGCG  540
             |||||||||||||| ||||| |||||||| |||||||||||| ||| || ||||||||
Sbjct  873   CGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGAGTGCTTAATGCG  814

Query  541   TTAACTTCCGCACTAAAGGACGGAAACCCTCTAACACTTACCACTCATCGTTTACGGCGG  600
             |||||||| |||||||||| |||||||||||||||||||| ||||||||||||||||||
Sbjct  813   TTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCATCGTTTACGGCGT  754

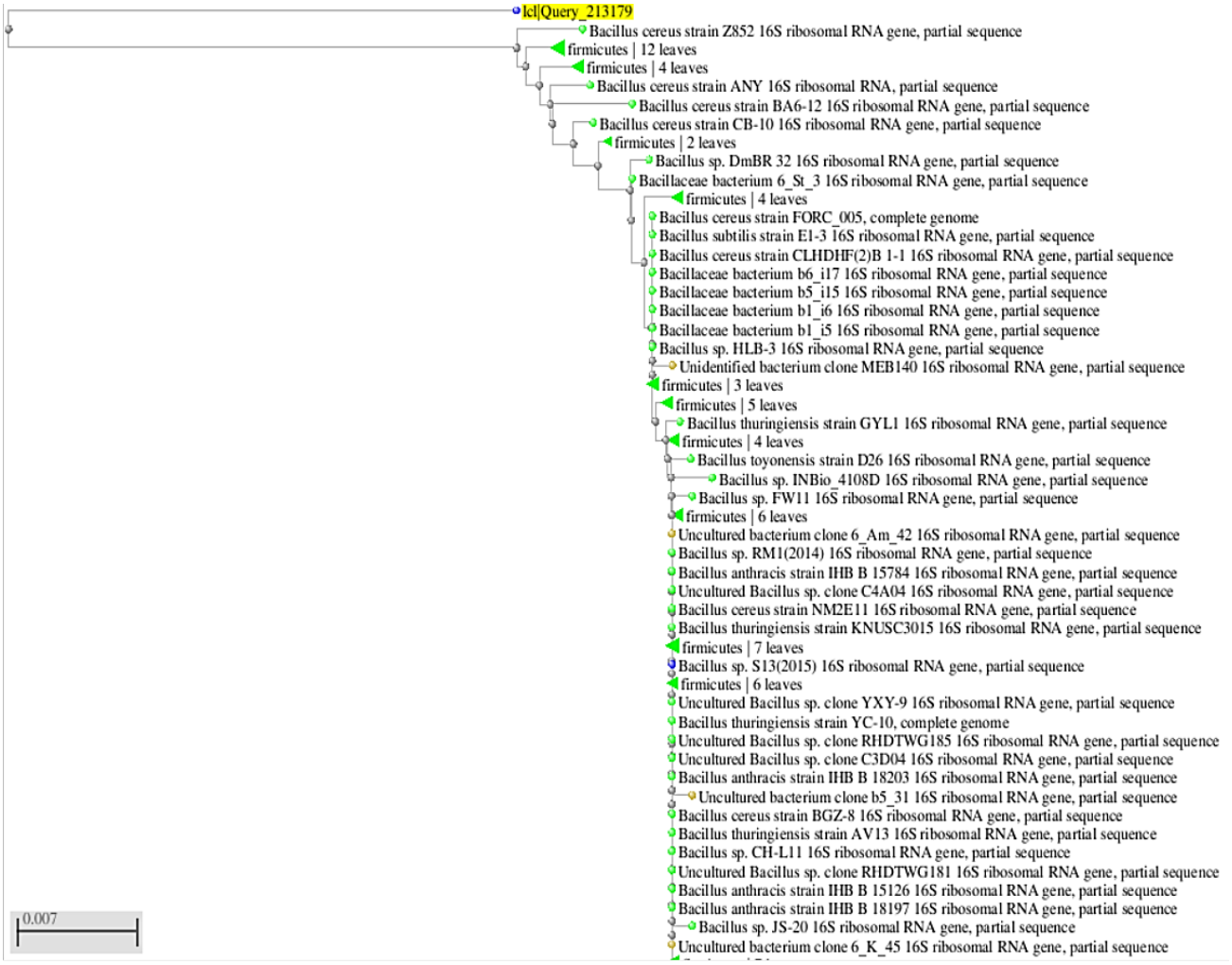
Query  601   GAACTACCAGGGTATCTAATCCGGTTTGCTCCCCACGCTTTCGCGCCTCACTGTCAGTTA  660
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  753   GAACTACCAGGGTATCTAATCCGGTTTGCTCCCCACGCTTTCGCGCCTCATTGTCAGTTA  694

Query  661   GAGACCAGAAAGTCCCCTTCGCCACTGGGGTTCCTCCATATCTCTACACATTTCACCGCT  720
              |||||| |||||| |||||||||||| |||||||||||||||||| ||||||||||||
Sbjct  693   CAGACCAAAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTACGCATTTCACCGCT  634

Query  721   ACCCATGAAATTCCACTTTCCTCATCTGCACTCAAATCTCCCAGTTTCCAATGACCCTCC  780
             || |||| |||||||||||||| |||||||||| |||||||||||||||||||||||||||
Sbjct  633   ACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCAGTTTCCAATGACCCTCC  574

Query  781   GGGGTTGACCCGGGGGCTTTCCCCTCAAACTTAAAAAACCACCTGCGCGCGCTTTACCCC  840
               |||||| ||| |||||||| | ||| |||||| ||||||||||||||||||||||||||
Sbjct  573   ACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACCTGCGCGCGCTTTACGCC  514

Query  841   C  841
             |
Sbjct  513   C  513
```


lcl|Query_213179
Bacillus cereus strain Z852 16S ribosomal RNA gene, partial sequence
firmicutes | 12 leaves
firmicutes | 4 leaves
Bacillus cereus strain ANY 16S ribosomal RNA, partial sequence
Bacillus cereus strain BA6-12 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain CB-10 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus sp. DmBR 32 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium 6_St_3 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Bacillus cereus strain FORC_005, complete genome
Bacillus subtilis strain E1-3 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain CLHDHF(2)B 1-1 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium b6_i17 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium b5_i15 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium b1_i6 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium b1_i5 16S ribosomal RNA gene, partial sequence
Bacillus sp. HLB-3 16S ribosomal RNA gene, partial sequence
Unidentified bacterium clone MEB140 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
firmicutes | 5 leaves
Bacillus thuringiensis strain GYL1 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Bacillus toyonensis strain D26 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4108D 16S ribosomal RNA gene, partial sequence
Bacillus sp. FW11 16S ribosomal RNA gene, partial sequence
firmicutes | 6 leaves
Uncultured bacterium clone 6_Am_42 16S ribosomal RNA gene, partial sequence
Bacillus sp. RM1(2014) 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 15784 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C4A04 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NM2E11 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain KNUSC3015 16S ribosomal RNA gene, partial sequence
firmicutes | 7 leaves
Bacillus sp. S13(2015) 16S ribosomal RNA gene, partial sequence
firmicutes | 6 leaves
Uncultured Bacillus sp. clone YXY-9 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain YC-10, complete genome
Uncultured Bacillus sp. clone RHDTWG185 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C3D04 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 18203 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone b5_31 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain BGZ-8 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain AV13 16S ribosomal RNA gene, partial sequence
Bacillus sp. CH-L11 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RHDTWG181 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 15126 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 18197 16S ribosomal RNA gene, partial sequence
Bacillus sp. JS-20 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 6_K_45 16S ribosomal RNA gene, partial sequence
0.007

Micrococcus luteus KT339390

Micrococcus luteus strain DYPSBB RPF YRP01 16S ribosomal RNA gene, partial sequence
Sequence ID: KT339390.1 **Length:** 1462 **Number of Matches:** 1

Range 1: 30 to 1424 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
2560 bits(1386)	0.0	1393/1396(99%)	2/1396(0%)	Plus/Plus

```
Query  2     ACATGCAAGTCGAACGATGAAGCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGT  61
Sbjct  30    ACATGCAAGTCGAACGATGAAGCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGT  89

Query  62    AACACGTGAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCTAATACCG  121
Sbjct  90    AACACGTGAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCTAATACCG  149

Query  122   GATAGGAGCGTCCACCGCATGGTGGGTGTTGGAAAGATTTATCGGTTTTGGATGGACTCG  181
Sbjct  150   GATAGGAGCGTCCACCGCATGGTGGGTGTTGGAAAGATTTATCGGTTTTGGATGGACTCG  209

Query  182   CGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCT  241
Sbjct  210   CGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCT  269

Query  242   GAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA  301
Sbjct  270   GAGAGGGTGACCGGCCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA  329

Query  302   GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACG  361
Sbjct  330   GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACG  389

Query  362   GCCTTCGGGTTGTAAACCTCTTTCAGTAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAA  421
Sbjct  390   GCCTTCGGGTTGTAAACCTCTTTCAGTAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAA  449

Query  422   GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCC  481
Sbjct  450   GAAGCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCC  509

Query  482   GGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTCGTGAAAGTCCGG  541
Sbjct  510   -GGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTCGTGAAAGTCCGG  568

Query  542   GGCTTAACCCCGGATCTGCGGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGA  601
Sbjct  569   GGCTTAACCCCGGATCTGCGGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGA  628

Query  602   ATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGG  661
Sbjct  629   ATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGG  688

Query  662   TCTCTGGGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGATTAGATAC  721
Sbjct  689   TCTCTGGGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGATTAGATAC  748

Query  722   CCTGGTAGTCCATGCCGTAAACGTTGGGCACTAGGTGTGGGGACCATTCCACGGTTTCCG  781
Sbjct  749   CCTGGTAGTCCATGCCGTAAACGTTGGGCACTAGGTGTGGGGACCATTCCACGGTTTCCG  808

Query  782   CGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCA  841
Sbjct  809   CGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCA  868

Query  842   AAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAACGCG  901
Sbjct  869   AAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAACGCG  928

Query  902   AAGAACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGAGATACGGTTTCCCCTTTG  961
Sbjct  929   AAGAACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGAGATACGGTTTCCCCTTTG  988

Query  962   GGGCGGGTTCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA  1021
Sbjct  989   GGGCGGGTTCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA  1048

Query  1022  GTCCCGCAACGAGCGCAACCCTCGTTCCATGTTGCCAGCACGTAATGGTGGGGACTCATG  1081
Sbjct  1049  GTCCCGCAACGAGCGCAACCCTCGTTCCATGTTGCCAGCACGTAATGGTGGGGACTCATG  1108

Query  1082  GGAGACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAATCATCATGCCCCTT  1141
Sbjct  1109  GGAGACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAATCATCATGCCCCTT  1168

Query  1142  ATGTCTTGGGCTTCACGCATGCTACAATGGCCGGTACAATGGGTTGCGATACTGTGAGGT  1201
Sbjct  1169  ATGTCTTGGGCTTCACGCATGCTACAATGGCCGGTACAATGGGTTGCGATACTGTGAGGT  1228

Query  1202  GGAGCTAATCCCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGA  1261
Sbjct  1229  GGAGCTAATCCCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGA  1288

Query  1262  AGTCGGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTT  1321
Sbjct  1289  AGTCGGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTT  1348

Query  1322  GTACACACCGCCCGTCAAGTCACGAAAGTTGGTAACACCCGAAGCCGGTGGCCTAACCCT  1381
Sbjct  1349  GTACACACCGCCCGTCAAGTCACGAAAGTTGGTAACACCCGAAGCCGGTGGCCTAACCCT  1408

Query  1382  TGTGGGGG-AGCCGTC  1396
Sbjct  1409  TGTGGGGGGAGCCGTC  1424
```


Micrococcus sp. 3442 16S ribosomal RNA gene, partial sequence
Micrococcus yunnanensis strain RWL-2 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3464 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 4 leaves
Micrococcus sp. PP1 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
high GC Gram+ | 3 leaves
high GC Gram+ | 2 leaves
Micrococcus sp. PP5 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3508 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 4 leaves
Micrococcaceae bacterium KVD-1921-02 16S ribosomal RNA gene, partial sequence
Micrococcus sp. WY3 16S ribosomal RNA gene, partial sequence
Micrococcus sp. SK57 gene for 16S rRNA, partial sequence
Micrococcus luteus strain VTM4R57 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate BF0001D063
Micrococcus sp. HEXBA04 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone MC01F04
Uncultured bacterium partial 16S rRNA gene, clone MC02C06
Micrococcaceae bacterium BQN1R-02d 16S ribosomal RNA gene, partial sequence
Micrococcaceae bacterium BQN1R-02d 16S ribosomal RNA gene, partial sequence
Micrococcus yunnanensis strain L7-617 16S ribosomal RNA gene, partial sequence
Micrococcus yunnanensis strain YIM 65004 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone TSJG-19 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
high GC Gram+ | 10 leaves
Micrococcus sp. M3T3B2 16S ribosomal RNA gene, partial sequence
Micrococcus sp. PX9_S1 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain JGTA-S5 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3517 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3498 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3308 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain VL-80 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain ChDC B378 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain IARI-IHD-5 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain KUDC1784 16S ribosomal RNA gene, partial sequence
Micrococcus sp. MN7-5 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000193 small subunit ribosomal RNA gene, partial sequence
high GC Gram+ | 7 leaves
high GC Gram+ | 2 leaves
high GC Gram+ | 17 leaves
Micrococcus luteus strain ex11 culture-collection CGMCC:7.112 16S ribosomal RNA gene, partial sequence
Micrococcus sp. JAM-AC11 gene for 16S rRNA, partial sequence
Micrococcus sp. PA-E028 16S ribosomal RNA gene, partial sequence
Bacterium BII-S5 partial 16S rRNA gene, isolate BII-S5
high GC Gram+ | 3 leaves
high GC Gram+ | 3 leaves
Micrococcus sp. A2-984 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3723 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SC04A11
high GC Gram+ | 4 leaves
0.0006

2- The phylogenetic analysis of bacteria isolated from mirror samples

Bacillus cereus KP100400.1

Bacillus cereus 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KP100400.1| **Length:** 1179 **Number of Matches:** 1

Range 1: 55 to 1014 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1683 bits(1866)	0.0	949/960(99%)	0/960(0%)	Plus/Plus

```
Query  1     GGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGGAAA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55    GGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGGAAA  114

Query  61    CCGGGGCTAATACCGGATAACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  115   CCGGGGCTAATACCGGATAACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCG  174

Query  121   GCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  175   GCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCA  234

Query  181   AGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  235   AGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  294

Query  241   CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGA  300
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  295   CCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGA  354

Query  301   GCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAAC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  355   GCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAAC  414

Query  361   AAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  415   AAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACT  474

Query  421   ACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTA  480
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  475   ACGTGCCAGCAGCCGCGGTAAAACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTA  534

Query  481   AAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCANCCGTGGAGGG  540
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  535   AAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGG  594

Query  541   TCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  595   TCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGT  654

Query  601   GAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  655   GAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTG  714

Query  661   ACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  715   ACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG  774

Query  721   TAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATT  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  775   TAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATT  834

Query  781   AAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  835   AAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCC  894

Query  841   CGCACAAGCGGGGGAGCATGTGGTTTAATTCGAAGCAACGCAAAAAACCTTACCAGGTCT  900
             |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  895   CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAAAACCTTACCAGGTCT  954

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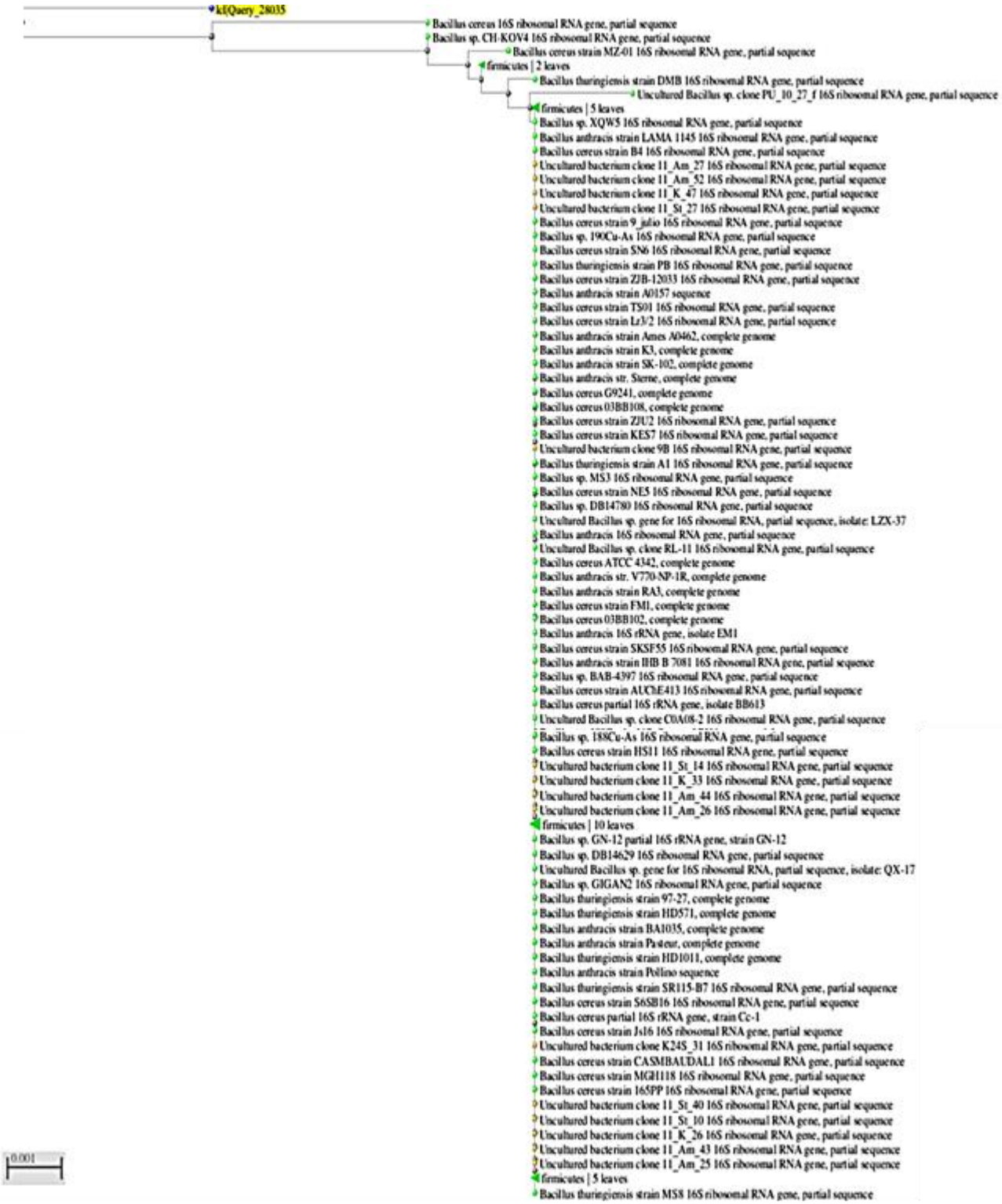
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Bacillus cereus 16S ribosomal RNA gene, partial sequence
Bacillus sp. CH-KOV4 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MZ-01 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus thuringiensis strain DMB 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone PU_10_27_f 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus sp. XQW5 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain LAMA 1145 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain B4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_52 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_K_47 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_27 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 9_julio 16S ribosomal RNA gene, partial sequence
Bacillus sp. 190Cu-As 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain SN6 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain PB 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain ZJB-12033 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain A0157 sequence
Bacillus cereus strain TS01 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain Lz3/2 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain Ames A0462, complete genome
Bacillus anthracis strain K3, complete genome
Bacillus anthracis strain SK-102, complete genome
Bacillus anthracis str. Sterne, complete genome
Bacillus cereus G9241, complete genome
Bacillus cereus 03BB108, complete genome
Bacillus cereus strain ZJU2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain KES7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 9B 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain A1 16S ribosomal RNA gene, partial sequence
Bacillus sp. MS3 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NE5 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14780 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: LZX-37
Bacillus anthracis 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RL-11 16S ribosomal RNA gene, partial sequence
Bacillus cereus ATCC 4342, complete genome
Bacillus anthracis str. V770-NP-1R, complete genome
Bacillus anthracis strain RA3, complete genome
Bacillus cereus strain FM1, complete genome
Bacillus cereus 03BB102, complete genome
Bacillus anthracis 16S rRNA gene, isolate EM1
Bacillus cereus strain SKSF55 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IIIB B 7081 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4397 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain AUCbE413 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, isolate BB613
Uncultured Bacillus sp. clone C0A08-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. 188Cu-As 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain HS11 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_14 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_K_33 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_44 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_26 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
Bacillus sp. GN-12 partial 16S rRNA gene, strain GN-12
Bacillus sp. DB14629 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: QX-17
Bacillus sp. GIGAN2 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain 97-27, complete genome
Bacillus thuringiensis strain HD571, complete genome
Bacillus anthracis strain BA1035, complete genome
Bacillus anthracis strain Pasteur, complete genome
Bacillus thuringiensis strain HD1011, complete genome
Bacillus anthracis strain Pollino sequence
Bacillus thuringiensis strain SR115-B7 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain S6SB16 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, strain Cc-1
Bacillus cereus strain Js16 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone K24S_31 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain CASMBAUDAL1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MGI1118 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 165PP 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_40 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_K_26 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_43 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_25 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus thuringiensis strain MS8 16S ribosomal RNA gene, partial sequence
0.001

Bacillus subtilis DQ683077.1

Bacillus subtilis strain GB03 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|DQ683077.1| **Length:** 1124 **Number of Matches:** 1

Range 1: 26 to 1004 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1739 bits(1928)	0.0	973/979(99%)	0/979(0%)	Plus/Plus

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Query  1    AGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTG  60
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Query  61   CCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCG  120
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Query  121  CATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATT  180
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Sbjct  146  CATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATT  205

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Sbjct  206  AGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTG  265

Query  241  ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAAT  300
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Sbjct  446  GTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGG  505

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Sbjct  506  CAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATG  565

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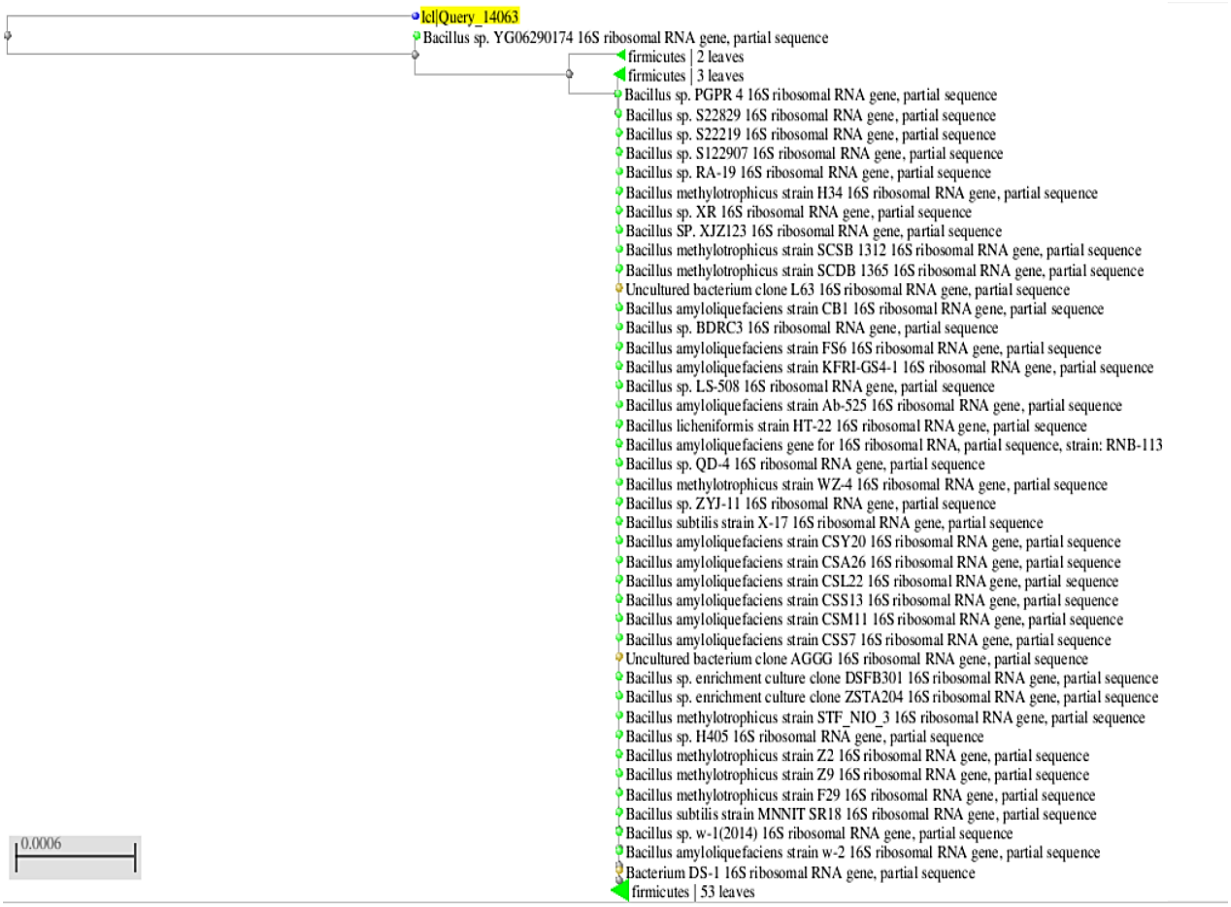
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firmicutes | 2 leaves
firmicutes | 3 leaves
Bacillus sp. PGPR 4 16S ribosomal RNA gene, partial sequence
Bacillus sp. S22829 16S ribosomal RNA gene, partial sequence
Bacillus sp. S22219 16S ribosomal RNA gene, partial sequence
Bacillus sp. S122907 16S ribosomal RNA gene, partial sequence
Bacillus sp. RA-19 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain H34 16S ribosomal RNA gene, partial sequence
Bacillus sp. XR 16S ribosomal RNA gene, partial sequence
Bacillus SP. XJZ123 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain SCSB 1312 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain SCDB 1365 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L63 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CB1 16S ribosomal RNA gene, partial sequence
Bacillus sp. BDRC3 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain FS6 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain KFRI-GS4-1 16S ribosomal RNA gene, partial sequence
Bacillus sp. LS-508 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain Ab-525 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain HT-22 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens gene for 16S ribosomal RNA, partial sequence, strain: RNB-113
Bacillus sp. QD-4 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain WZ-4 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZYJ-11 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain X-17 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSY20 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSA26 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSL22 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSS13 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSM11 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain CSS7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone AGGG 16S ribosomal RNA gene, partial sequence
Bacillus sp. enrichment culture clone DSFB301 16S ribosomal RNA gene, partial sequence
Bacillus sp. enrichment culture clone ZSTA204 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain STF_NIO_3 16S ribosomal RNA gene, partial sequence
Bacillus sp. H405 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain Z2 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain Z9 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain F29 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MNNIT SR18 16S ribosomal RNA gene, partial sequence
Bacillus sp. w-1(2014) 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain w-2 16S ribosomal RNA gene, partial sequence
Bacterium DS-1 16S ribosomal RNA gene, partial sequence
firmicutes | 53 leaves
0.0006

Bacillus cereus JQ659737.1

Bacillus cereus strain R5-339 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|JQ659737.1| Length: 1492 Number of Matches: 1

Range 1: 100 to 1025 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1631 bits(1808)	0.0	918/926(99%)	1/926(0%)	Plus/Plus

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Sbjct  160   GCTAATACCGGATAACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGCTTCGGCTGT  219

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Query  241   CTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAAC  300
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Sbjct  340   CTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAAC  399

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Sbjct  400   GCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAGAACAAGTG  459

Query  361   CTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTG  420
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Sbjct  460   CTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTG  519

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Sbjct  580   CGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATT  639

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Sbjct  820   GATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATTAAGCA  879

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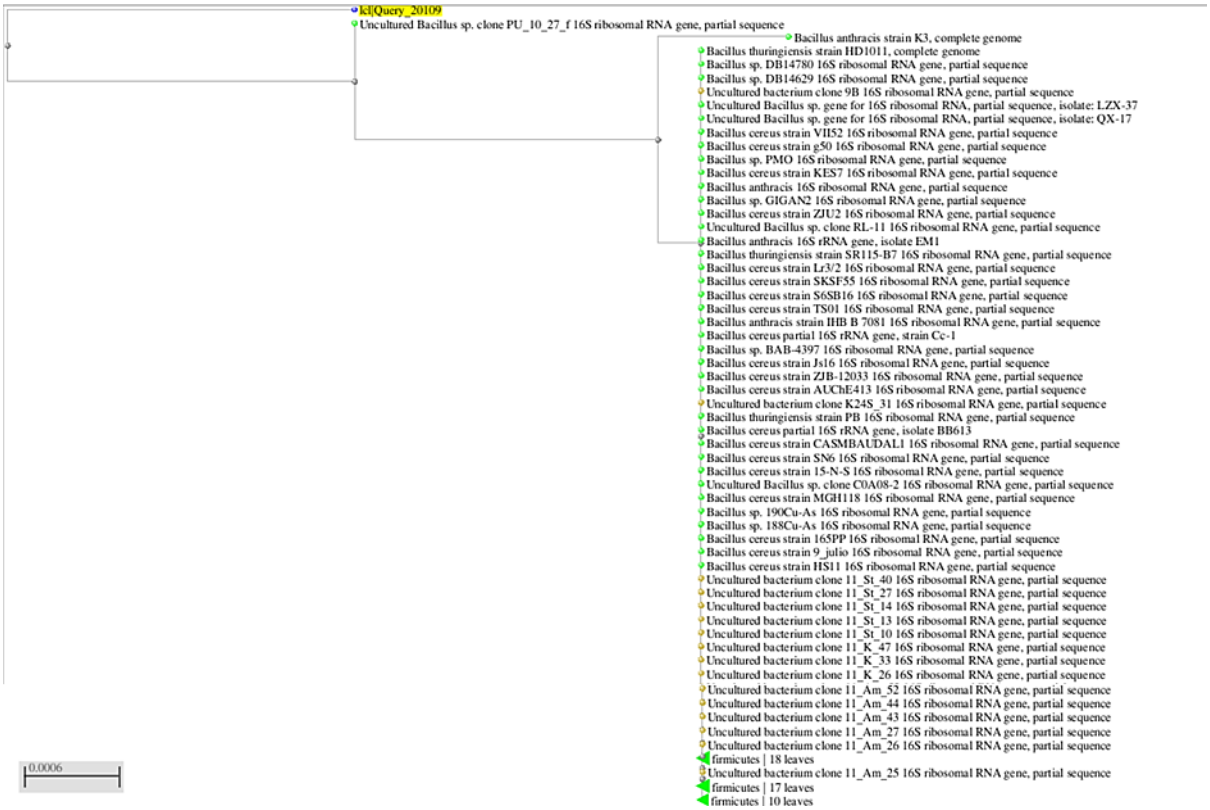
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Uncultured Bacillus sp. clone PU_10_27_f 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain K3, complete genome
Bacillus thuringiensis strain HD1011, complete genome
Bacillus sp. DB14780 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14629 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 9B 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: LZX-37
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: QX-17
Bacillus cereus strain VII52 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain g50 16S ribosomal RNA gene, partial sequence
Bacillus sp. PMO 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain KES7 16S ribosomal RNA gene, partial sequence
Bacillus anthracis 16S ribosomal RNA gene, partial sequence
Bacillus sp. GIGAN2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain ZJU2 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RL-11 16S ribosomal RNA gene, partial sequence
Bacillus anthracis 16S rRNA gene, isolate EM1
Bacillus thuringiensis strain SR115-B7 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain Lr3/2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain SKSF55 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain S6SB16 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain TS01 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 7081 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, strain Cc-1
Bacillus sp. BAB-4397 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain Js16 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain ZJB-12033 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain AUChE413 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone K24S_31 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain PB 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, isolate BB613
Bacillus cereus strain CASMBAUDAL1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain SN6 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 15-N-S 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C0A08-2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MGH118 16S ribosomal RNA gene, partial sequence
Bacillus sp. 190Cu-As 16S ribosomal RNA gene, partial sequence
Bacillus sp. 188Cu-As 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 16SPP 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 9_julio 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain HS11 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_40 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_14 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_13 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_St_10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_K_47 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone 11_Am_27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 11_Am_26 16S ribosomal RNA gene, partial sequence
firmicutes | 18 leaves
Uncultured bacterium clone 11_Am_25 16S ribosomal RNA gene, partial sequence
firmicutes | 17 leaves
firmicutes | 10 leaves
0.0006

Staphylococcus haemolyticus KC139455.1

Staphylococcus haemolyticus strain B-20 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KC139455.1| **Length:** 1428 **Number of Matches:** 1

Range 1: 508 to 1366 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
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Sbjct  1246  CAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTACCCTTTGTATTGTCCATTGTAG  1187

Query  181   CACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1186  CACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCC  1127

Query  241   GGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1126  GGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGG  1067

Query  301   GTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1066  GTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGC  1007

Query  361   ACCACCTGTCACTTTGTCCCCCGAAGGGGAAAGCTCTATCTCTAGAGTTGTCAAAGGATG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1006  ACCACCTGTCACTTTGTCCCCCGAAGGGGAAAGCTCTATCTCTAGAGTTGTCAAAGGATG  947

Query  421   TCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT  480
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Sbjct  946   TCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT  887

Query  481   GCGGGTCCCCGTCAATTCCTTTGAGTTTCANNCTTGCGNTCGTACTCCCCAGGCGGAGTG  540
             |||||||||||||||||||||||||||||  |||||| ||||||||||||||||||||||
Sbjct  886   GCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTG  827

Query  541   CTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGN  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  826   CTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGT  767

Query  601   TTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACNCTTTCGCACATCAG  660
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  766   TTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACGCTTTCGCACATCAG  707

Query  661   CGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCAT  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  706   CGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTGCGCAT  647

Query  721   TTCACCGCTACACATGGAAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTTTCCA  780
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  646   TTCACCGCTACACATGG-AATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAGTTTCCA  588

Query  781   ATGACCCTCCACGGTTGAGCCGTGGGCTTTCCCATCCGACTTAAAAAACCGCCTACGCGC  840
             |||||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||
Sbjct  587   ATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAAAAACCGCCTACGCGC  528

Query  841   GCCTTTACGCCCAATAAATTCC  862
             | |||||||||||||| ||||||
Sbjct  527   G-CTTTACGCCCAAT-AATTCC  508
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lcl|Query_33409
Human oral bacterium C20 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain Hb-6 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain B-17 16S ribosomal RNA gene, partial sequence
Staphylococcus petrasii subsp. pragensis strain CCM 8529 16S ribosomal RNA gene, partial sequence
Staphylococcus petrasii subsp. croceilyticus strain MCC11690 16S ribosomal RNA gene, partial sequence
Bacterium NLAE-zl-P566 16S ribosomal RNA gene, partial sequence
Staphylococcus petrasii subsp. pragensis strain LMG 28328 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain HNS011 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain B-20 16S ribosomal RNA gene, partial sequence
Staphylococcus jettensis strain SEQ257 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Staphylococcus aureus strain 254/Chen 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 383/Chen 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain Pn1016/Pant-Uttar/2007 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus subsp. aureus 11819-97, complete genome
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000357 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000535 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0178-T478-S-NIPCRAMgANa_000494 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000170 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000319 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000573 small subunit ribosomal RNA gene, partial sequence
Staphylococcus aureus subsp. aureus strain XJYL-M6-1 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain B-16 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain Z221 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain Z1092 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. SR24-1 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 179 (BC31(B)) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus subsp. aureus strain 92B (BSJ3) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 129A (BC40Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 140A (bc2) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 15 (BC19) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 29 (BR56) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 74 (br12) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 94A (br8) 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. ChDC B590 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 2RM0Y1 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain IS 1/2 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain RW-302 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus subsp. aureus DNA, complete genome, strain: TMUS2134
Staphylococcus aureus strain OUC_Est2S 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus genome assembly NCTC13435, chromosome : 1
Staphylococcus aureus strain NF4 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain CICC 10384 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain LJH-Y1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. SB-3 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 89A (BR66) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 42 (C2TJ) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 158B (BR61Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 147B (BR64Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 130A (BR68) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 102 (BR65Fs(A)) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 124B (BC38Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain O2 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain C123 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain Z1261 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain KIBGE-IB24 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain G18 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000628 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000444 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000178 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000011 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0175-T455-S-NIPCRAMgANa_000843 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000359 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000082 small subunit ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Staphylococcus haemolyticus strain Sh29/312/L2, complete genome
Staphylococcus aureus subsp. aureus DNA, complete genome, strain: TMUS2126
Staphylococcus aureus subsp. aureus ST772-MRSA-V strain DAR4145, complete genome
Staphylococcus haemolyticus strain GZSP-3 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain AMRF2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. BAB-3242 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 89B (BR66) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 48 (br14) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 166A (BR60Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 148B (BC39Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 139B (br27) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 118A (BR69Ms) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain 115B (BR67Fs) 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus subsp. aureus CN1, complete genome
Staphylococcus aureus strain C126 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain Z1263 16S ribosomal RNA gene, partial sequence
Staphylococcus aureus strain Z222 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. N2 partial 16S rRNA gene, strain N2
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000662 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000500 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000310 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000107 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0177-T472-S-NIPCRAMgANa_000516 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000382 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000321 small subunit ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Staphylococcus aureus strain RKI4, complete genome
0.0009

3- The phylogenetic analysis of bacteria isolated from computer Keyboards and computer mice samples

Bacillus subtilis KJ746466.1

Bacillus subtilis strain ACHSOC779 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ746466.1| **Length:** 1266 **Number of Matches:** 1

Range 1: 14 to 970 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1701 bits(1886)	0.0	952/957(99%)	1/957(0%)	Plus/Plus

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Query  1    CTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14   CTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATA  73

Query  61   ACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACATAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   ACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACATAAA  133

Query  121  AGGTGGCTTYGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTA  180
            |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  AGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTA  193

Query  181  ACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  ACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  253

Query  241  TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAA  313

Query  301  AGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  AGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  373

Query  361  TAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  TAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGC  433

Query  421  CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434  CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  493

Query  481  TATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  494  TATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCA  553

Query  541  ACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554  ACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCA  613

Query  601  CGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  614  CGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTG  673

Query  661  GTCTGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  674  GTCTGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT  733

Query  721  AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  734  AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCA  793

Query  781  GCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAAT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  794  GCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAAT  853

Query  841  TGAC-GGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACC  899
            ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  854  TGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACC  913

Query  900  TTACCCGGTCTTGACATCCTCTGACATCCTAAAAATAGGACGTCCCCTTCGGGGGCA  956
            |||||  |||||||||||||||||||||||||  | ||||||||||||||||||||||
Sbjct  914  TTACCAGGTCTTGACATCCTCTGACATCCTAGAGATAGGACGTCCCCTTCGGGGGCA  970
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lcl|Query_18947
Bacillus sp. SSKSD11 16S ribosomal RNA gene, partial sequence
Bacillus sp. V4 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain WZ-3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain B11 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SAU-Ab-9 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain L11 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain BMP01 16S ribosomal RNA gene, partial sequence
Bacillus sp. VITNJ2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain AY02 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain GTG-69 16S ribosomal RNA gene, partial sequence
Bacterium NF2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain GG62 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SCKB1444 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SCSB1461 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis gene for 16S rRNA, partial sequence, strain: 33-1
Bacillus tequilensis gene for 16S rRNA, partial sequence, strain: 142-2
Bacillus subtilis strain CH12 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain CH16 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Bp-1 16S ribosomal RNA, partial sequence
Bacillus sp. ZLXH-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-6 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Natto3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PPL-S11 16S ribosomal RNA gene, partial sequence
Bacillus sp. HE08 16S ribosomal RNA gene, partial sequence
Bacterium Y2 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ44 16S ribosomal RNA gene, partial sequence
Bacillus sp. CEB332.1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SANN3 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ121 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ43 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DL47 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PPL-SC9 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Lys-1249 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain jk-45 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain IHB B 7075 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain IC3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain CH13 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone SA2 16S ribosomal RNA gene, partial sequence
firmicutes | 20 leaves
Bacillus subtilis subsp. subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain RAS-1 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ45 16S ribosomal RNA gene, partial sequence
firmicutes | 36 leaves
Bacillus subtilis strain W6 16S ribosomal RNA gene, partial sequence
0.0006

Bacillus amyloliquefaciens AB301004.1

Bacillus amyloliquefaciens gene for 16S rRNA, partial sequence, strain: GH3

Sequence ID: dbj|AB301004.1| **Length:** 1481 **Number of Matches:** 1

Range 1: 447 to 1408 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1709 bits(1894)	0.0	957/962(99%)	1/962(0%)	Plus/Minus

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Query  1     GTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACC  60
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Sbjct  1408  GTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACC  1349

Query  61    GCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTG  120
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Sbjct  1348  GCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTG  1289

Query  121   CGATCCGAACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTTT  180
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Sbjct  1288  CGATCCGAACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTTT  1229

Query  181   GTTCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC  240
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Sbjct  1228  GTTCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC  1169

Query  241   ATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTG  300
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Sbjct  1168  ATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTG  1109

Query  301   GCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAG  360
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Sbjct  1108  GCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAG  1049

Query  361   CTGACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATCTCTAGG  420
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Sbjct  1048  CTGACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATCTCTAGG  989

Query  421   ATTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACAT  480
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Sbjct  988   ATTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACAT  929

Query  481   GCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACT  540
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Sbjct  928   GCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACT  869

Query  541   CCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACAC  600
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Sbjct  868   CCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACAC  809

Query  601   TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACG  660
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Sbjct  808   TTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACG  749

Query  661   CTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  748   CTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCC  689

Query  721   ACATCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGT  780
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Sbjct  688   ACATCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGT  629

Query  781   TCCCCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAA  840
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Sbjct  628   TCCCCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAA  569

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Sbjct  568   CCGCCTGCGAGCCCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACC  509

Query  901   GCGGCTGCTGGCACGTAGTTAGCCG-GGCTTTCTGGTTAGGTACCGTCAAGGGGCCCCCC  959
             ||||||||||||||||||||||||| |||||||||||||||||||||||||||| ||| |||
Sbjct  508   GCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCCGCCC  449

Query  960   TA  961
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Sbjct  448   TA  447
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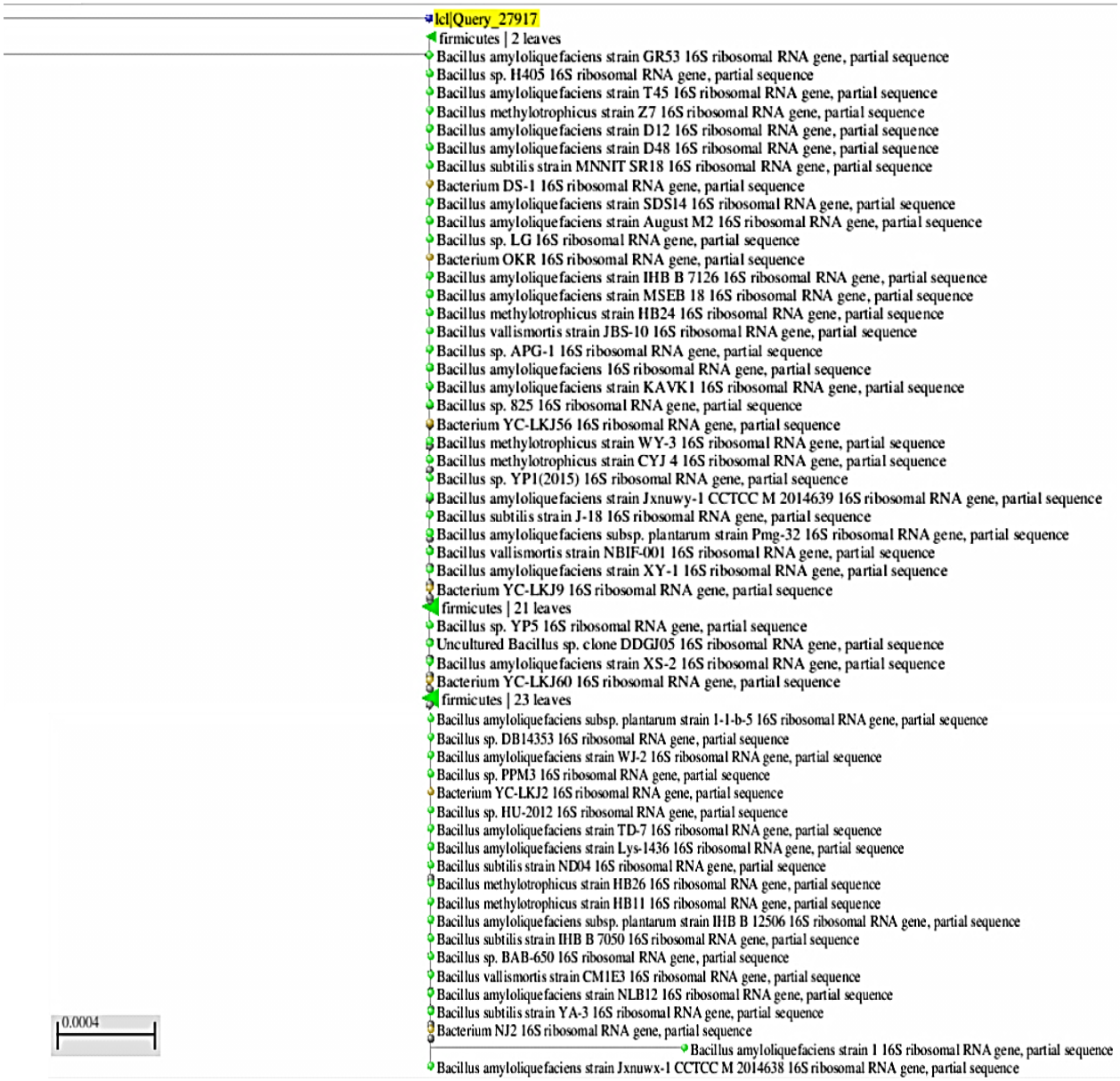
lcl|Query_27917
firmicutes | 2 leaves
Bacillus amyloliquefaciens strain GR53 16S ribosomal RNA gene, partial sequence
Bacillus sp. H405 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain T45 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain Z7 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain D12 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain D48 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MNNIT SR18 16S ribosomal RNA gene, partial sequence
Bacterium DS-1 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain SDS14 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain August M2 16S ribosomal RNA gene, partial sequence
Bacillus sp. LG 16S ribosomal RNA gene, partial sequence
Bacterium OKR 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain IHB B 7126 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain MSEB 18 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain HB24 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain JBS-10 16S ribosomal RNA gene, partial sequence
Bacillus sp. APG-1 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain KAVK1 16S ribosomal RNA gene, partial sequence
Bacillus sp. 825 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ56 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain WY-3 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain CYJ 4 16S ribosomal RNA gene, partial sequence
Bacillus sp. YP1(2015) 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain Jxnuwy-1 CCTCC M 2014639 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain J-18 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens subsp. plantarum strain Pmg-32 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain NBIF-001 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain XY-1 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ9 16S ribosomal RNA gene, partial sequence
firmicutes | 21 leaves
Bacillus sp. YP5 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone DDGJ05 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain XS-2 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ60 16S ribosomal RNA gene, partial sequence
firmicutes | 23 leaves
Bacillus amyloliquefaciens subsp. plantarum strain 1-1-b-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14353 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain WJ-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. PPM3 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ2 16S ribosomal RNA gene, partial sequence
Bacillus sp. HU-2012 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain TD-7 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain Lys-1436 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain ND04 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain HB26 16S ribosomal RNA gene, partial sequence
Bacillus methylotrophicus strain HB11 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens subsp. plantarum strain IHB B 12506 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain IHB B 7050 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-650 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain CM1E3 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain NLB12 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain YA-3 16S ribosomal RNA gene, partial sequence
Bacterium NJ2 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain 1 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain Jxnuwx-1 CCTCC M 2014638 16S ribosomal RNA gene, partial sequence
0.0004

Brevibacillus brostelensis EU816699.1

Brevibacillus borstelensis clone US12 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|EU816699.1| **Length:** 1529 **Number of Matches:** 1

Range 1: 93 to 1053 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1656 bits(1836)	0.0	946/962(98%)	2/962(0%)	Plus/Plus

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Query  1     GTAACACGTAGGCAACCTGCCCGTAAGCTCGGGATAACATGGGGAAACTCATGCTAATAC  60
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Sbjct  93    GTAACACGTAGGCAACCTGCCCGTAAGCTCGGGATAACATGGGGAAACTCATGCTAATAC  152

Query  61    CGGATAGGGTCTTCTCTCGCATGAGAGGAGACGGAAAGGTGGCGCAAGCTACCACTTACG  120
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  153   CGGATAGGGTCTTCTCTCGCATGAGGGGAGACGGAAAGGTGGCGCAAGCTACCACTTACG  212

Query  121   GATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  213   GATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCG  272

Query  181   TAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  273   TAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACG  332

Query  241   GGAGGCAGCAGTAGGGAATTTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTG  300
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Sbjct  333   GGAGGCAGCAGTAGGGAATTTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTG  392

Query  301   AACGATGAAGGTCTTCGGATTGTAAAGTTCTGTTGTCAGAGACGAACAAGTACCGTTCGA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  393   AACGATGAAGGTCTTCGGATTGTAAAGTTCTGTTGTCAGAGACGAACAAGTACCGTTCGA  452

Query  361   ACAGGGCGGTACCTTGACGGTACCTGACGAGAAAGCCACGGCTAACTACGTGCCAGCAGC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  453   ACAGGGCGGTACCTTGACGGTACCTGACGAGAAAGCCACGGCTAACTACGTGCCAGCAGC  512

Query  421   CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGG  480
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  513   CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAGGCGCGCGCAGG  572

Query  481   CGGCTATGTAAGTCTGGTGTTAAAGCCCGGGGCTCAACCCCGGTTCGCATCGGAAACTGT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  573   CGGCTATGTAAGTCTGGTGTTAAAGCCCGGGGCTCAACCCCGGTTCGCATCGGAAACTGT  632

Query  541   GTAGCTTGAGTGCAGAAGAGGAAAGCGGTATTCCACGTGTAGCGGTGAAATGCGTAGAGA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  633   GTAGCTTGAGTGCAGAAGAGGAAAGCGGTATTCCACGTGTAGCGGTGAAATGCGTAGAGA  692

Query  601   TGTGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGTCTGTAACTGACGCTGAGGCGCGA  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  693   TGTGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGTCTGTAACTGACGCTGAGGCGCGA  752

Query  661   AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  753   AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGC  812

Query  721   TAGGTGGTgggggggTTTCAATACCCTCAGTGCCGCAGCTAACGCAATAAGCACTCCGCC  780
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  813   TAGGTGGTTGGGGGGTTTCAATACCCTCAGTGCCGCAGCTAACGCAATAAGCACTCCGCC  872

Query  781   TGGGGAGTACGCTCGCAAGAGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGG  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  873   TGGGGAGTACGCTCGCAAGAGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGT  932

Query  841   GGAGCATGGGGTTTAATTCGAAGCAACGCGAAGAACCTTACCA-GTCTTGACATCCCGCT  899
             |||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  933   GGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGCT  992

Query  900   GACCGTCCTAAAAATAGGGCTTCCCTTCGGGGCAGCGGGGAAgggggggggggATGGTGGT  959
             |||||||||| | |||||||||||||||||||||||| | |   || || | ||||| ||
Sbjct  993   GACCGTCCTAGAGATAGGGCTTCCCTTCGGGGCAGCGGTG-ACAGGTGGTGCATGGTTGT  1051

Query  960   CG  961
             ||
Sbjct  1052  CG  1053
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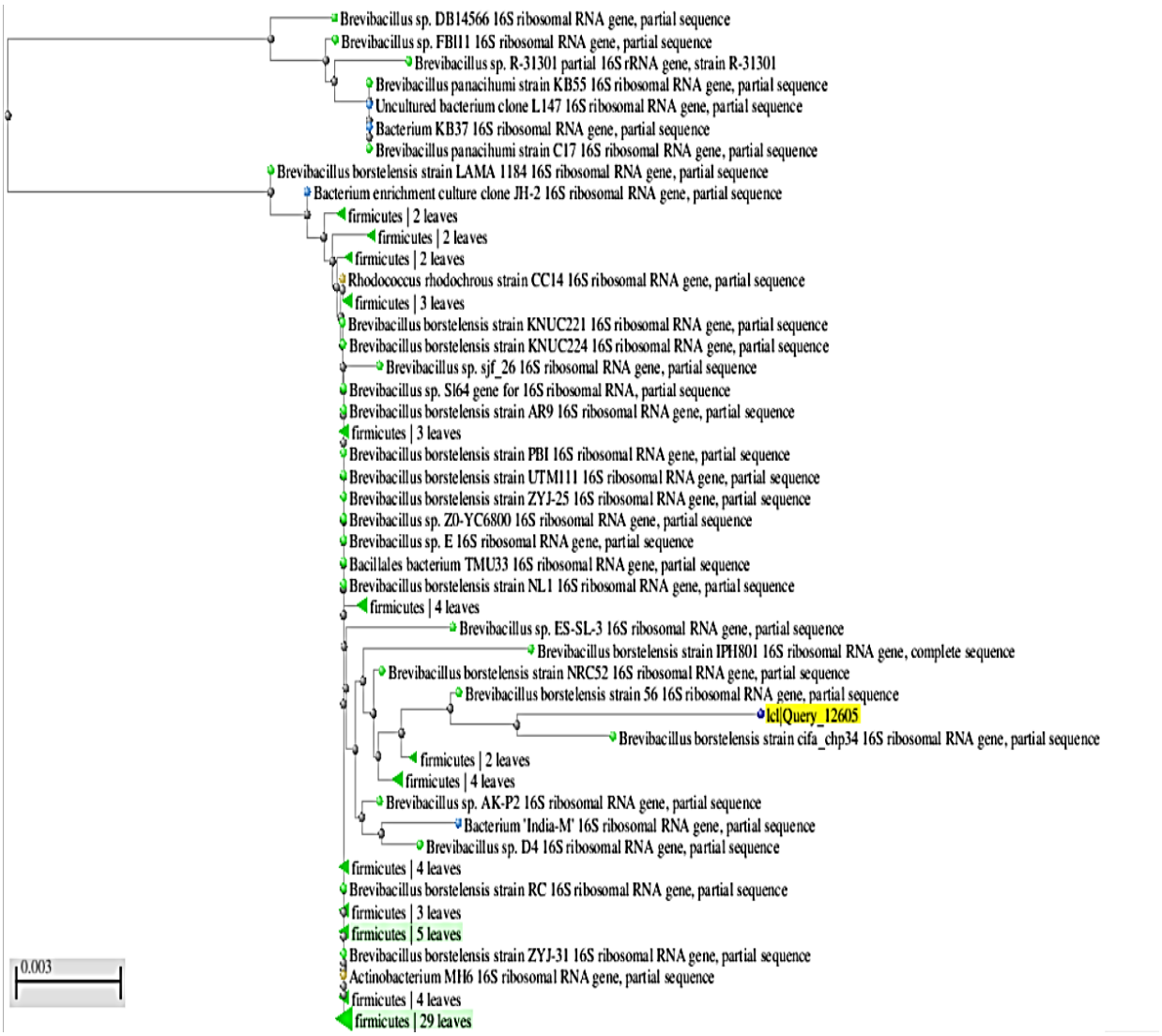
Brevibacillus sp. DB14566 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. FBI11 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. R-31301 partial 16S rRNA gene, strain R-31301
Brevibacillus panacihumi strain KB55 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L147 16S ribosomal RNA gene, partial sequence
Bacterium KB37 16S ribosomal RNA gene, partial sequence
Brevibacillus panacihumi strain C17 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain LAMA 1184 16S ribosomal RNA gene, partial sequence
Bacterium enrichment culture clone JH-2 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 2 leaves
firmicutes | 2 leaves
Rhodococcus rhodochrous strain CC14 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Brevibacillus borstelensis strain KNUC221 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain KNUC224 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. sjf_26 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. Sl64 gene for 16S ribosomal RNA, partial sequence
Brevibacillus borstelensis strain AR9 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Brevibacillus borstelensis strain PBI 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain UTM111 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain ZYJ-25 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. Z0-YC6800 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. E 16S ribosomal RNA gene, partial sequence
Bacillales bacterium TMU33 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain NL1 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Brevibacillus sp. ES-SL-3 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain IPH1801 16S ribosomal RNA gene, complete sequence
Brevibacillus borstelensis strain NRC52 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain 56 16S ribosomal RNA gene, partial sequence
lcl|Query_12605
Brevibacillus borstelensis strain cifa_chp34 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 4 leaves
Brevibacillus sp. AK-P2 16S ribosomal RNA gene, partial sequence
Bacterium 'India-M' 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. D4 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Brevibacillus borstelensis strain RC 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
firmicutes | 5 leaves
Brevibacillus borstelensis strain ZYJ-31 16S ribosomal RNA gene, partial sequence
Actinobacterium MH6 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
firmicutes | 29 leaves
0.003

Staphylococcus epidermidis KF575163.1

Staphylococcus epidermidis strain G0242 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF575163.1| **Length:** 1434 **Number of Matches:** 1

Range 1: 44 to 1016 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1718 bits(1904)	0.0	967/973(99%)	3/973(0%)	Plus/Plus

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  44    TTGACGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTACCTATAAGACTGGGATA  103

Query  61    ACTTCGGGAAACCGGAGCTAATACCGGATAATATTTCGAACCGCATGGTTCGATAGTGAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  104   ACTTCGGGAAACCGGAGCTAATACCGGATAATATTTCGAACCGCATGGTTCGATAGTGAA  163

Query  121   AGATGGTTTTGCTATCACTTATAGATGGACCCGCGCCGTATTAGCTAGTTGGTAAGGTAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164   AGATGGTTTTGCTATCACTTATAGATGGACCCGCGCCGTATTAGCTAGTTGGTAAGGTAA  223

Query  181   CGGCTTACCAAGGCGACGATACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  224   CGGCTTACCAAGGCGACGATACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACT  283

Query  241   GAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  284   GAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAA  343

Query  301   GCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  344   GCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATT  403

Query  361   AGGGAAGAACATACGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  404   AGGGAAGAACATACGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCA  463

Query  421   CGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTAT-CCGGAATT  479
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  464   CGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCCGGAATT  523

Query  480   ATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAA  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  524   ATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAA  583

Query  540   CCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAT  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  584   CCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAT  643

Query  600   GTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGG  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  644   GTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGG  703

Query  660   TCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTA  719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  704   TCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTA  763

Query  720   GTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAG  779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  764   GTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAG  823

Query  780   CTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATT  839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  824   CTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATT  883

Query  840   GACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGC-ACGCGAAAAACCT  898
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||||
Sbjct  884   GACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCT  943

Query  899   TACCAAATCTTGACATCCTTTGACAACTCTAAAGATAGAGCCTTCCCCTTTCGGGGGA-A  957
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |
Sbjct  944   TACCAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCCTTCCCCTTTCGGGGGACA  1003

Query  958   AAGTGACAGGGGG  970
             ||||||||||| ||
Sbjct  1004  AAGTGACAGGTGG  1016
```


kl|Query_218737
Uncultured bacterium clone nck172b01c1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain G0242 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain Sh29/312/L2, complete genome
Staphylococcus sp. BQN2P-01d 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbu277a09c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbu283c12c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbu283g02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw830e11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw831h11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1189e10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1095d07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1105h02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1106f08c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1106h08c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1107b10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1108c04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1065c02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1189f06c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1191b10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1190f12c1 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain LCR51 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain EQI12 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain FR1_68 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd558b09c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd577e07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd836b11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd983f02c1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. YSL09-4 gene for 16S rRNA, partial sequence
Uncultured bacterium clone ncd924b12c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd1271c06c1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. HL-13 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain CIFRI D-TSB2 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain CIFRI P-TSB4 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CIFRI CH-TSB23 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CIFRI H-TSB-15-ZMA 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CIFRI H-TSB-20-ZMA 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CIFRI H-TSB-6-HA 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain HNMCTR1 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain BP3_2B 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain LEH2_2A 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. EB338 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone TJ-3 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. ARB1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 20.1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 21.1 16S ribosomal RNA gene, partial sequence
Acinetobacter radioresistens strain G16 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain G35 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. RH-29 gene for 16S rRNA, partial sequence
Staphylococcus sp. M17 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus JCSC1435 strain JCSC1435 16S ribosomal RNA, complete sequence
Staphylococcus haemolyticus strain M2 16S ribosomal RNA gene, partial sequence
Bacterium CulaenoE10F 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain S001N 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain S006N 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain S009b 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain S011b 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain VBW023 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_182 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain L38 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain BP/SU2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. H-179 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain SH6 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain SH8 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain NIOT-sb3 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain C0181 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. G0271 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain PAH-3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone g3b23 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone g3b26 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone g3b27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone g3b33 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone g3b39 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain XB20 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain MJMG7.10 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain KJ1-5-97 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain KJ1599 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck176a12c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck170f04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck171d06c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncm50e05c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncm50g10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck169d07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck171g08c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck175c09c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck177d11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck188e05c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck310c02c1 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain DG-4 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain CIFRI P-TSB-72 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain J12 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 09-A3 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 09-M3 16S ribosomal RNA gene, partial sequence
Staphylococcus haemolyticus strain DSO4G14 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Ag08 16S ribosomal RNA gene, partial sequence
Bacterium 7RO1 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Staphylococcus haemolyticus strain DSO6G11 16S ribosomal RNA gene, partial sequence

Pantoea caldia AB907785.1

Pantoea calida gene for 16S ribosomal RNA, partial sequence, strain: LMG 25383

Sequence ID: dbj|AB907785.1| **Length:** 1495 **Number of Matches:** 1

Range 1: 51 to 1032 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1745 bits(1934)	0.0	977/982(99%)	1/982(0%)	Plus/Plus

```
Query  1     AGCAGCTTGCTGCTTCGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGGATCTGCCC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  51    AGCAGCTTGCTGCTTCGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGGATCTGCCC  110

Query  61    GATGGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAACGTCGCAAGACCAAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  111   GATGGAGGGGGATAACCACTGGAAACGGTGGCTAATACCGCATAACGTCGCAAGACCAAA  170

Query  121   GTGGGGGACCTTCGGGCCTCACACCATCGGATGAACCCAGATGGGATTAGCTAGTAGGTG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171   GTGGGGGACCTTCGGGCCTCACACCATCGGATGAACCCAGATGGGATTAGCTAGTAGGTG  230

Query  181   GGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACT  240
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Sbjct  231   GGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACT  290

Query  241   GGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGG  300
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Sbjct  291   GGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGG  350

Query  301   GCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  351   GCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACT  410

Query  361   TTCAGCGGGGAGGAAGGGATGGTGCTTAATACGCGCCGTCATTGACGTTACCCGCAGAAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  411   TTCAGCGGGGAGGAAGGGATGGTGCTTAATACGCGCCGTCATTGACGTTACCCGCAGAAG  470

Query  421   AAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCG  480
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Sbjct  471   AAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCG  530

Query  481   GAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531   GAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGG  590

Query  541   CTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAAT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  591   CTTAACCTGGGAACTGCATTTGAAACTGGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAAT  650

Query  601   TCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  711   CCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  770

Query  721   TGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGCTGTTTCCTTGAGAAGTGGCTTCC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  771   TGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGCTGTTTCCTTGAGAAGTGGCTTCC  830

Query  781   GGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATG  840
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Sbjct  831   GGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATG  890

Query  841   AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGA  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  891   AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGA  950

Query  901   ACCTTACCTGGTCTTGACATCCACGGAATTCGGCAAAAATGCCCTAGTGCCTTCGGGAAC  960
             |||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
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Sbjct  1011  CGTGAGACAGGTGCTGCATGGC  1032
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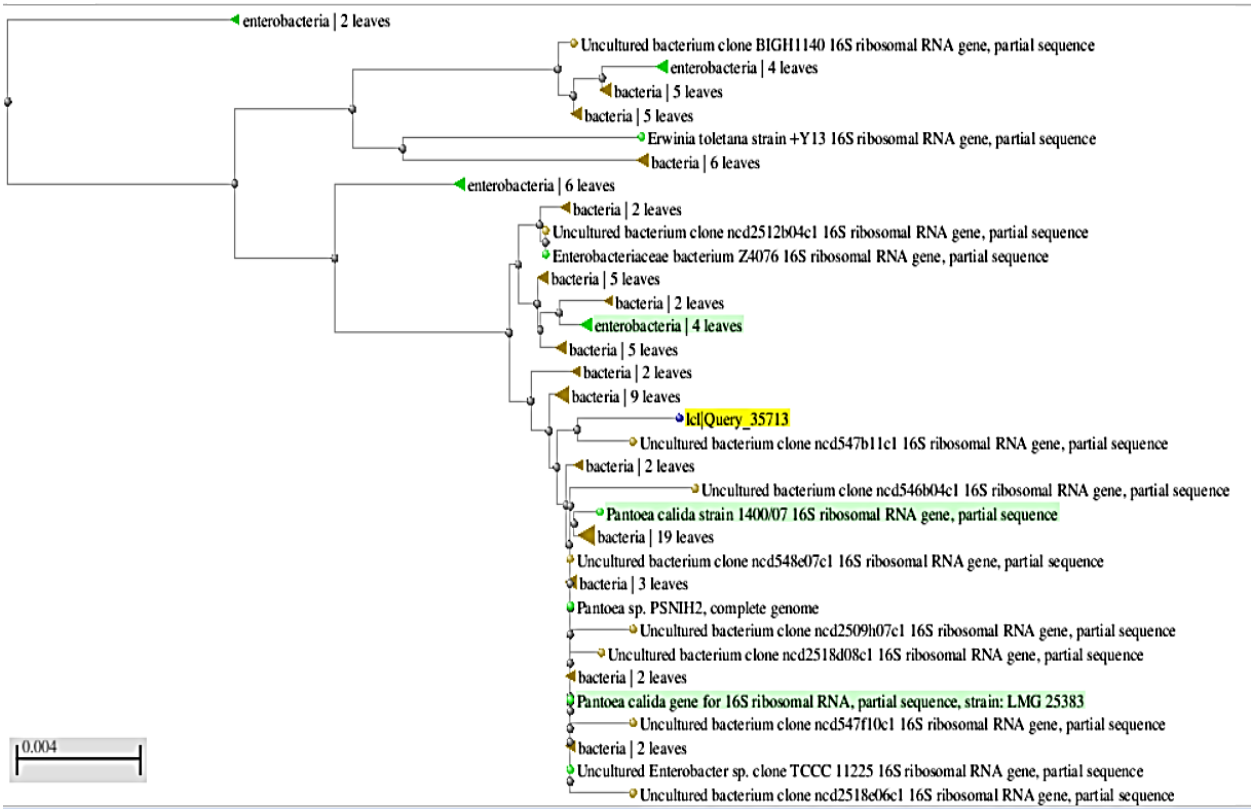
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Uncultured bacterium clone BIGH1140 16S ribosomal RNA gene, partial sequence
enterobacteria | 4 leaves
bacteria | 5 leaves
bacteria | 5 leaves
Erwinia toletana strain +Y13 16S ribosomal RNA gene, partial sequence
bacteria | 6 leaves
enterobacteria | 6 leaves
bacteria | 2 leaves
Uncultured bacterium clone ncd2512b04c1 16S ribosomal RNA gene, partial sequence
Enterobacteriaceae bacterium Z4076 16S ribosomal RNA gene, partial sequence
bacteria | 5 leaves
bacteria | 2 leaves
enterobacteria | 4 leaves
bacteria | 5 leaves
bacteria | 2 leaves
bacteria | 9 leaves
lcl|Query_35713
Uncultured bacterium clone ncd547b11c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Uncultured bacterium clone ncd546b04c1 16S ribosomal RNA gene, partial sequence
Pantoea calida strain 1400/07 16S ribosomal RNA gene, partial sequence
bacteria | 19 leaves
Uncultured bacterium clone ncd548e07c1 16S ribosomal RNA gene, partial sequence
bacteria | 3 leaves
Pantoea sp. PSNIH2, complete genome
Uncultured bacterium clone ncd2509h07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2518d08c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Pantoea calida gene for 16S ribosomal RNA, partial sequence, strain: LMG 25383
Uncultured bacterium clone ncd547f10c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Uncultured Enterobacter sp. clone TCCC 11225 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2518e06c1 16S ribosomal RNA gene, partial sequence
0.004

Bacillus cereus DQ923480.1

Bacillus cereus strain D23 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|DQ923480.1| **Length:** 1429 **Number of Matches:** 1

Range 1: 430 to 1390 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1725 bits(1912)	0.0	959/961(99%)	0/961(0%)	Plus/Minus

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Sbjct  1390  TGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCG  1331

Query  61    CGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTAC  120
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Sbjct  1330  CGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTAC  1271

Query  121   AATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTG  180
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Sbjct  1270  AATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTG  1211

Query  181   TACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA  240
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Sbjct  1210  TACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA  1151

Query  241   TCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGG  300
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Sbjct  1150  TCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGG  1091

Query  301   CAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGC  360
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Sbjct  1090  CAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGC  1031

Query  361   TGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGG  420
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Sbjct  1030  TGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGG  971

Query  421   TTTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATG  480
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Sbjct  970   TTTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATG  911

Query  481   CTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  910   CTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTC  851

Query  541   CCCAGGCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACT  600
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Query  601   TAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC  660
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Sbjct  790   TAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGC  731

Query  661   TTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCA  720
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Sbjct  730   TTTCGCGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCA  671

Query  721   TATCTCTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  670   TATCTCTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTC  611

Query  781   TCCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAAACTTAAGAAA  840
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Sbjct  610   TCCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAA  551

Query  841   CCACCTGCGCGCGCTTTACGCCCAATAATTTCCGGATAACGCTTGCCACCTACGTATTAC  900
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Sbjct  550   CCACCTGCGCGCGCTTTACGCCCAATAATTTCCGGATAACGCTTGCCACCTACGTATTAC  491

Query  901   CGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGGGCCAGC  960
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Sbjct  490   CGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCCAGC  431

Query  961   T  961
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Sbjct  430   T  430
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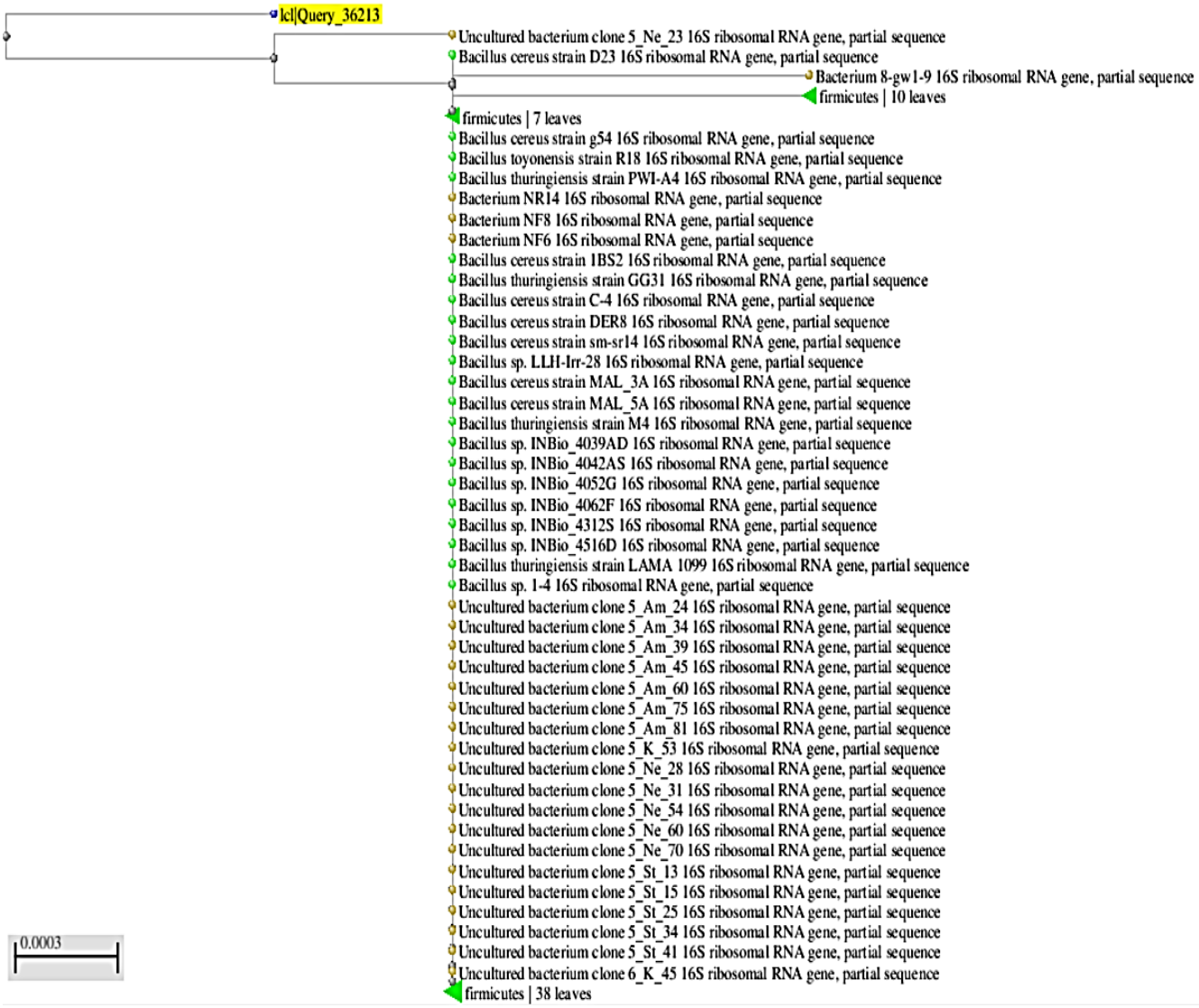
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Bacillus cereus strain D23 16S ribosomal RNA gene, partial sequence
Bacterium 8-gw1-9 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
firmicutes | 7 leaves
Bacillus cereus strain g54 16S ribosomal RNA gene, partial sequence
Bacillus toyonensis strain R18 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain PWI-A4 16S ribosomal RNA gene, partial sequence
Bacterium NR14 16S ribosomal RNA gene, partial sequence
Bacterium NF8 16S ribosomal RNA gene, partial sequence
Bacterium NF6 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 1BS2 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain GG31 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain C-4 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain DER8 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain sm-sr14 16S ribosomal RNA gene, partial sequence
Bacillus sp. LLH-Irr-28 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MAL_3A 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MAL_5A 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain M4 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4039AD 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4042AS 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4052G 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4062F 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4312S 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4516D 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain LAMA 1099 16S ribosomal RNA gene, partial sequence
Bacillus sp. 1-4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_24 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_34 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_39 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_45 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_60 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_75 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_81 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_K_53 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_28 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_31 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_54 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_60 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_70 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_13 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone 5_St_25 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_34 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_41 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 6_K_45 16S ribosomal RNA gene, partial sequence
firmicutes | 38 leaves
0.0003

Pseudomonas luteola KC429633.1

Pseudomonas luteola strain XFB-BV 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KC429633.1| **Length:** 1388 **Number of Matches:** 1

Range 1: 42 to 991 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1669 bits(1850)	0.0	940/950(99%)	0/950(0%)	Plus/Plus

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Sbjct  42   GGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGAAAG  101

Query  61   GAACGCTAATACCGCATACGTCCTACGGGAGAAAGTGGGGGATCTTCGGACCTCACGCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GAACGCTAATACCGCATACGTCCTACGGGAGAAAGTGGGGGATCTTCGGACCTCACGCTA  161

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Sbjct  162  TCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCGACGAT  221

Query  181  CCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCT  240
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Query  241  ACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGC  300
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Sbjct  402  TAATACGTTGCAGCTTTGACGTTACCAGCAGAATAAGCACCGGCTAACTCTGTGCCAGCA  461

Query  421  GCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTA  480
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Sbjct  462  GCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTA  521

Query  481  GGTGGCTTGGTAAGTTGAATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAAC  540
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Query  601  ATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTG  660
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Query  661  CGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTC  720
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Sbjct  702  CGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTC  761

Query  721  AACTAGCCGTTGGGGTCCTTGAGACTTTAGTGGCGCAGCTAACGCAATAAGTTGACCGCC  780
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Query  901  AACTTTCCAAAAAAGGATTGGTGCCTTCGGGAACTCTGAACCAGGGGCTG  950
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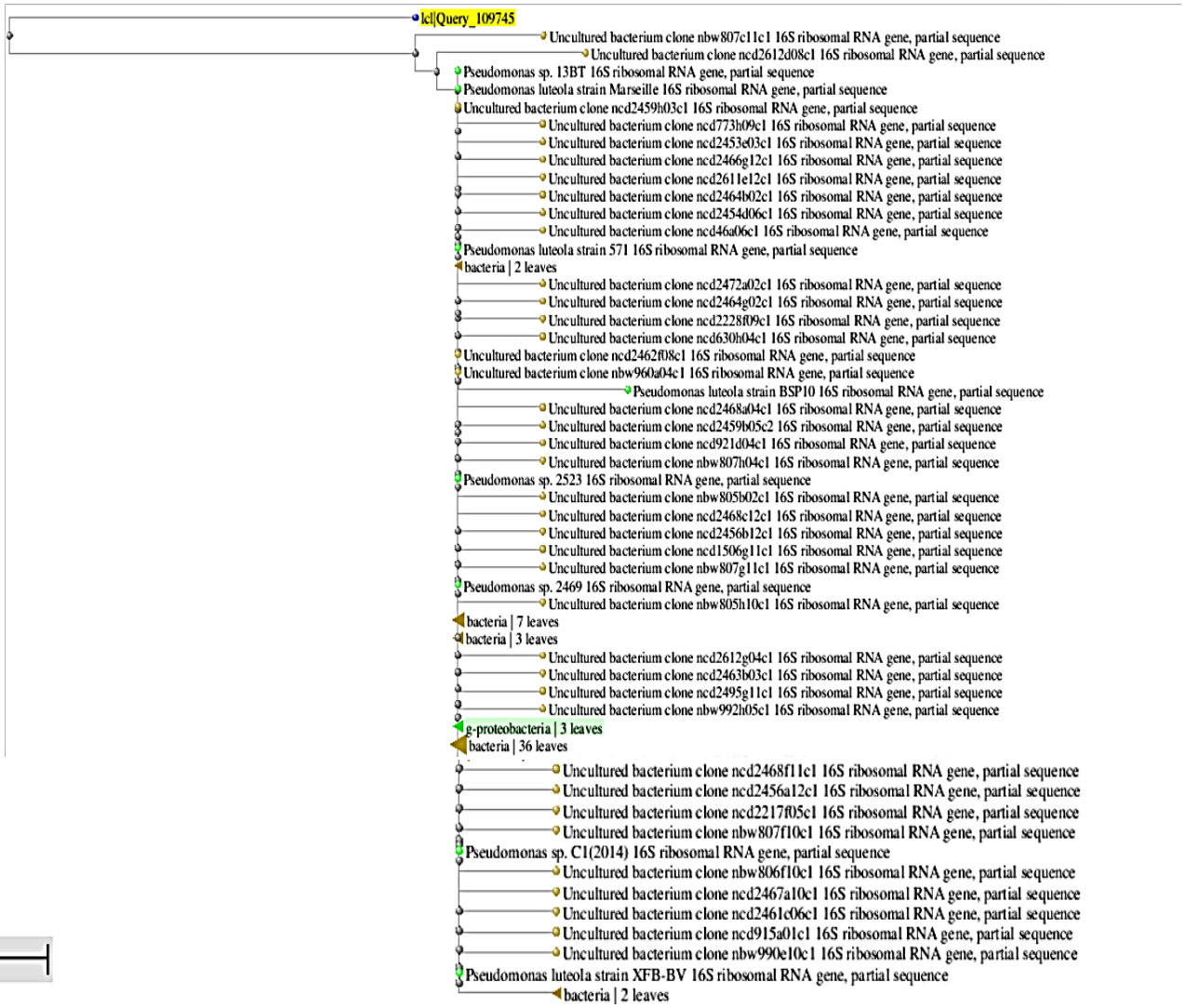
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Uncultured bacterium clone ncd2612d08c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 13BT 16S ribosomal RNA gene, partial sequence
Pseudomonas luteola strain Marseille 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2459h03c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd773h09c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2453e03c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2466g12c1 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone ncd2464b02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2454d06c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd46a06c1 16S ribosomal RNA gene, partial sequence
Pseudomonas luteola strain 571 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Uncultured bacterium clone ncd2472a02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2464g02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2228f09c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd630h04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2462f08c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw960a04c1 16S ribosomal RNA gene, partial sequence
Pseudomonas luteola strain BSP10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2468a04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2459b05c2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd921d04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw807h04c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 2523 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw805b02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2468c12c1 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone nbw807g11c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 2469 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw805h10c1 16S ribosomal RNA gene, partial sequence
bacteria | 7 leaves
bacteria | 3 leaves
Uncultured bacterium clone ncd2612g04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2463b03c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2495g11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw992h05c1 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 3 leaves
bacteria | 36 leaves
Uncultured bacterium clone ncd2468f11c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2456a12c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2217f05c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw807f10c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. C1(2014) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw806f10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2467a10c1 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone ncd915a01c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw990e10c1 16S ribosomal RNA gene, partial sequence
Pseudomonas luteola strain XFB-BV 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
0.001

4- The phylogenetic analysis of bacteria isolated from mobile phones samples

Staphylococcus epidermidis KJ398217.1

Staphylococcus epidermidis strain LH-Y4 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ398217.1| **Length:** 1413 **Number of Matches:** 1

Range 1: 590 to 1369 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1398 bits(1550)	0.0	778/780(99%)	0/780(0%)	Plus/Minus

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Query  3     CTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCT  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1369  CTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCT  1310

Query  63    GATCTACGATTACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAAC  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1309  GATCTACGATTACTAGCGATTCCAGCTTCATATAGTCGAGTTGCAGACTACAATCCGAAC  1250

Query  123   TGAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTACCCTTTGTATTGTCCA  182
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1249  TGAGAACAACTTTATGGGATTTGCTTGACCTCGCGGTTTCGCTGCCCTTTGTATTGTCCA  1190

Query  183   TTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCT  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1189  TTGTAGCACGTGTGTAGCCCAAATCATAAGGGGCATGATGATTTGACGTCATCCCCACCT  1130

Query  243   TCCTCCGGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGC  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1129  TCCTCCGGTTTGTCACCGGCAGTCAACTTAGAGTGCCCAACTTAATGATGGCAACTAAGC  1070

Query  303   TTAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAA  362
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Sbjct  1069  TTAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAA  1010

Query  363   CCATGCACCACCTGTCACTCTGTCCCCCGAAGGGGAAAACTCTATCTCTAGAGGGGTCAG  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1009  CCATGCACCACCTGTCACTCTGTCCCCCGAAGGGGAAAACTCTATCTCTAGAGGGGTCAG  950

Query  423   AGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  949   AGGATGTCAAGATTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC  890

Query  483   GCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGC  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  889   GCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGC  830

Query  543   GGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  829   GGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACT  770

Query  603   CATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACGCTTTCGCA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  769   CATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGATCCCCACGCTTTCGCA  710

Query  663   CATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  709   CATCAGCGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCT  650

Query  723   GCGCATTTCACCGCTACACATGGAAATTCCACTTTCGTCTTCTGCACTCAAGTTTTCCAG  782
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  649   GCGCATTTCACCGCTACACATGGAAATTCCACTTTCCTCTTCTGCACTCAAGTTTTCCAG  590
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kl|Query_53347
Bacterium N47 16S ribosomal RNA gene, partial sequence
Bacterium N47 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Staphylococcus epidermidis strain Y5 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain JDM2_4A 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain LEH7_1A 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain ECNU-UE2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain ECNU-UI1 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0023-T100-S-NIPCRAMgANb_000153 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000053 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000167 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000384 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0072-T477-S-NIPCRAMgANa_000465 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000009 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000108 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000382 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000517 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000534 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0178-T478-S-NIPCRAMgANa_000084 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000049 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000054 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000085 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000101 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000378 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0026-T115-S-NIPCRAMgANa_000491 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0028-T175-S-NIPCRAMgANa_000053 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000297 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000440 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000548 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000554 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000563 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000564 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000076 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000155 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000193 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000217 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000397 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000425 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000467 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000482 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000549 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0041-T385-S-NIPCRAMgANb_000188 small subunit ribosomal RNA gene, partial sequence
Staphylococcus epidermidis gene for 16S ribosomal RNA, partial sequence, isolate: B0619
Staphylococcus epidermidis strain S9-627 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain M-S-MRS_6 16S ribosomal RNA gene, partial sequence
Bacterium NLAE-zl-G470 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain XJFH-J-1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis partial 16S rRNA gene, isolate 0609ALT19Q2-GH
Staphylococcus epidermidis strain HKG 163 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. EllikeE4 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain HKG 182 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain HKG 183 16S ribosomal RNA gene, partial sequence
Bacterium L-20 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone C139100025 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. W2.10-181 16S ribosomal RNA (16S rRNA) gene, complete sequence
Staphylococcus epidermidis strain 72 (br3) 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain ATHA24 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. DF7n-C small subunit ribosomal RNA gene, partial sequence
Staphylococcus epidermidis partial 16S rRNA gene, isolate OCAT7
Staphylococcus epidermidis partial 16S rRNA gene, isolate OCAT8
Staphylococcus sp. OCAT10 partial 16S rRNA gene, isolate OCAT10
Staphylococcus epidermidis partial 16S rRNA gene, isolate OCAT31
Staphylococcus epidermidis partial 16S rRNA gene, isolate OCAT33
Staphylococcus epidermidis partial 16S rRNA gene, isolate OCOB9
Staphylococcus epidermidis strain Au22 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain B7_3CO2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. QD53 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis partial 16S rRNA gene, strain JPR-05
Uncultured bacterium clone Ap.ba-F-DM-HN-1-27 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain W 3/4 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain W+5/13 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. PJRI24 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis PM221 complete genome
Staphylococcus epidermidis strain ASI 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain C18 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain SEI, complete genome
Staphylococcus sp. RJ7 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. JPR7 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain P 1/1 16S ribosomal RNA gene, partial sequence
Bacterium EM-2014-133 genomic DNA containing 16S-23S intergenic spacer region, isolate 133
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: smkt_Fir_002_002
firmicutes | 3 leaves

Staphylococcus warneri KP771665.1

Staphylococcus warneri strain SuMS_N03 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KP771665.1| **Length:** 1463 **Number of Matches:** 1

Range 1: 112 to 563 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
807 bits(894)	0.0	450/452(99%)	0/452(0%)	Plus/Plus

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Query  5    ACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGG  64
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Sbjct  112  ACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGG  171

Query  65   ATAACCCATTGAACCGCATGGTTCAATAGTGAAAGGCGGCTTTGCTGTCACTTATAGATG  124
            |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172  ATAACATATTGAACCGCATGGTTCAATAGTGAAAGGCGGCTTTGCTGTCACTTATAGATG  231

Query  125  GATCCGCGCCGTATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATACGTAGC  184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  232  GATCCGCGCCGTATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATACGTAGC  291

Query  185  CGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAG  244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  292  CGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAG  351

Query  245  GCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTG  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  352  GCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTG  411

Query  305  ATGAAGGTCTTCGGATCGTAAAACTCTGTTATCAGGGAAGAACAAATGTGTAAGTAACTG  364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  412  ATGAAGGTCTTCGGATCGTAAAACTCTGTTATCAGGGAAGAACAAATGTGTAAGTAACTG  471

Query  365  TGCACATCTTGACGGTACCTGATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGG  424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  472  TGCACATCTTGACGGTACCTGATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGG  531

Query  425  TAATACGTAGGTGGCAAGCGTTATCCGGAATT  456
            ||||||||||||||||||||||||||||||||
Sbjct  532  TAATACGTAGGTGGCAAGCGTTATCCGGAATT  563
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lcl|Query_64441
Staphylococcus sp. HL73 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Iso-16 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. partial 16S rRNA gene, isolate BA-141
Staphylococcus warneri strain 40A 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri SG1 strain SG1 16S ribosomal RNA, complete sequence
Staphylococcus warneri strain 11BP 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone H 05 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone H 26 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone H 28 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain CS11 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain SCSIO 04349 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain 7.06EO2 16S ribosomal RNA gene, partial sequence
Bacterium LGM64 16S ribosomal RNA gene, partial sequence
Bacterium LGM94 16S ribosomal RNA gene, partial sequence
Bacterium LGM96 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. MRSE4 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. EllikeE5 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain CE83 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. C10b 16S ribosomal RNA gene, partial sequence
Staphylococcus sp.C10c strain C10c 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain 11W6FMR22 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain y357 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain SCD2-4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B24-203 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain X66 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain Z52 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain M2C2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain N7API2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain 171B (BR11-15) 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain BTDF2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: OM-C_C06
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: OM-U_B01
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: OM-U_D01
Staphylococcus sp. HFB0021 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain Co11 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone PF34-58 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Act36 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain 81b 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain MJMG7.13 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri partial 16S rRNA gene, isolate N25
Staphylococcus warneri partial 16S rRNA gene, isolate N16
Staphylococcus warneri partial 16S rRNA gene, isolate N17
Staphylococcus warneri partial 16S rRNA gene, isolate N33
Staphylococcus sp. P34 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. AK-4 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain LH-Ka3 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone DMV_ASJ2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 8-1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 8-2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 28-4 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 9-7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw890d01c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw898f04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1181c01c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck25c10c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck31d06c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd1392b01c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncm65d05c1 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. gene for 16S ribosomal RNA, partial sequence, clone: DhS1-5
Staphylococcus sp. EP_S_84 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri genomic DNA containing 16S-23S intergenic spacer region, strain NiB
Bacterium SCSIO13300 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. enrichment culture clone zhuowei 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. PMS08 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain RJ24 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain CS.B10 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. MY-CA13 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. MY-CA92 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: LpF35_1
firmicutes | 31 leaves

Bacillus subtilis HG764646.1

Bacillus subtilis partial 16S rRNA gene, isolate C737

Sequence ID: emb|HG764646.1| **Length:** 995 **Number of Matches:** 1

Range 1: 13 to 951 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1656 bits(1836)	0.0	931/939(99%)	1/939(0%)	Plus/Minus

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Query  1    CTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTA  60
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Sbjct  951  CTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTA  892

Query  61   TTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  891  TTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGC  832

Query  121  AGACTGCGATCCGAACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  831  AGACTGCGATCCGAACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTG  772

Query  181  CCCTTTGTTCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTT  240
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Sbjct  771  CCCTTTGTTCTGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTT  712

Query  241  GACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGA  300
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Sbjct  711  GACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGA  652

Query  301  ATGCTGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGA  360
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Sbjct  651  ATGCTGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGA  592

Query  361  CACGAGCTGACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATC  420
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Sbjct  591  CACGAGCTGACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATC  532

Query  421  TCTAGGATTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAA  480
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Sbjct  531  TCTAGGATTGTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAA  472

Query  481  CCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGAC  540
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Sbjct  471  CCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGAC  412

Query  541  CGTACTCCCCANGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCC  600
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  411  CGTACTCCCCAGGCGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCC  352

Query  601  TAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  351  TAACACTTAGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTC  292

Query  661  CCCACGCTTTCGCTCCTCAGCGTCAGTTACAGANCAGAGAGTCGCCTTCGCCACTGGTGT  720
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Sbjct  291  CCCACGCTTTCGCTCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGT  232

Query  721  TCCTCCACATCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCAC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  TCCTCCACATCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCAC  172

Query  781  TCAAGTTCCCCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACT  840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  171  TCAAGTTCCCCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACT  112

Query  841  TAAAAAACCGCCTGCGAGCCCTTTACGCCCAATAATTCCCGGA-AACGCTTGCCCCCTAC  899
            ||| |||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  111  TAAGAAACCGCCTGCGAGCCCTTTACGCCCAATAATTCCCGGACAACGCTTGCCACCTAC  52

Query  900  GTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTT  938
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Sbjct  51   GTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTT  13
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lcl|Query_13695
Bacillus sp. WP-XY19-3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis partial 16S rRNA gene, isolate C737
Bacillus tequilensis strain RBEB6 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis strain Z36S 16S ribosomal RNA gene, partial sequence
Bacillus sp. K6-15P 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens gene for 16S rRNA, partial sequence, strain: CSP
Bacillus tequilensis strain 111-4 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain YNA13 16S ribosomal RNA gene, complete sequence
Bacillus tequilensis strain BE-1A 16S ribosomal RNA gene, partial sequence
Bacillus sp. DC3158 16S ribosomal RNA gene, partial sequence
Bacillus sp. HYC-1-3 16S ribosomal RNA gene, partial sequence
Bacillus sp. JR65 16S ribosomal RNA gene, partial sequence
Bacillus sp. JR64 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PEBS07031802 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain ASAG1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain 1778 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain DJ-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone Zhuo1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DC2-2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain QD399 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain B6-1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain A9 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone Hswb-29 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain ADG 2 16S ribosomal RNA gene, partial sequence
Bacterium L3 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Azospirillum lipoferum partial 16S rRNA gene, isolate 17:1
Bacillus subtilis strain H32 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
firmicutes | 2 leaves
firmicutes | 5 leaves
Bacillus subtilis subsp. spizizenii strain AB4 16S ribosomal RNA gene, partial sequence
Bacillus subtilis KCTC 1028, complete genome
Bacillus subtilis subsp. subtilis strain 3NA, complete genome
Bacillus subtilis strain PS832, complete genome
Bacillus subtilis subsp. subtilis str. 168, complete genome
Bacillus subtilis subsp. subtilis str. AG1839, complete genome
Bacillus subtilis subsp. subtilis str. JH642 substr. AG174, complete genome
Bacillus subtilis subsp. subtilis 6051-HGW, complete genome
Bacillus subtilis subsp. subtilis str. AG1839, complete genome
Bacillus subtilis subsp. subtilis str. JH642 substr. AG174, complete genome
Bacillus subtilis subsp. subtilis 6051-HGW, complete genome
Bacillus subtilis XF-1, complete genome
Bacillus subtilis BEST7003 DNA, complete genome
Bacillus subtilis BEST7613 DNA, complete genome
Uncultured bacterium clone Hswb-2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. subtilis str. 168 complete genome
Bacillus sp. ARBELICrg 16S ribosomal RNA gene, partial sequence
Bacillus sp. VP 18 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain M-11 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ44 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ45 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ43 16S ribosomal RNA gene, partial sequence
Bacillus sp. KHR-38 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens partial 16S rRNA gene, isolate NBtR-1
Bacterium Y2 16S ribosomal RNA gene, partial sequence
Bacillus sp. 825 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ121 16S ribosomal RNA gene, partial sequence
firmicutes | 35 leaves

Bacillus cereus KJ612539.1

Bacillus cereus strain EM13 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ612539.1| **Length:** 1397 **Number of Matches:** 1

Range 1: 431 to 1378 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1660 bits(1840)	0.0	941/951(99%)	3/951(0%)	Plus/Minus

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Query  1     GTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGC  60
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Sbjct  1378  GTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGC  1319

Query  61    GGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACA  120
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Sbjct  1318  GGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACA  1259

Query  121   ATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGT  180
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Sbjct  1258  ATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGT  1199

Query  181   ACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1198  ACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT  1139

Query  241   CCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  CCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGC  1079

Query  301   AACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCT  360
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Sbjct  1078  AACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCT  1019

Query  361   GACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGGT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  GACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGGT  959

Query  421   TTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGC  480
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Sbjct  958   TTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGC  899

Query  481   TCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCC  540
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Sbjct  898   TCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCC  839

Query  541   CCAGGCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  838   CCAGGCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTT  779

Query  601   AGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  778   AGCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCT  719

Query  661   TTCGCGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCAT  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  718   TTCGCGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCAT  659

Query  721   ATCTCTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCT  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  658   ATCTCTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCT  599

Query  781   CCCAGTTTCCAATGACCCTCCACGGGTTGAGCCGTGGGCTTTCACATCAAAGTTAAAAAA  840
             |||||||||||||||||||||| |||||||||||||||||||||| | |||| |||
Sbjct  598   CCCAGTTTCCAATGACCCTCCAC-GGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAA  540

Query  841   CCACCTGCGCGCGCTTTACGCCCAATAATTCCCGGAAAACGCTTGCCCCCTACGTATTAC  900
             |||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Sbjct  539   CCACCTGCGCGCGCTTTACGCCCAATAATTCCCGGATAACGCTTGCCACCTACGTATTAC  480

Query  901   CGCGGCTGCTGGCACGTAATTAGCCGGGGCTTTCCTGGTTAAGGTACCGTC  951
             |||||||||||||||||| ||||||| |||||| |||||| ||||||||||
Sbjct  479   CGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTT-CTGGTT-AGGTACCGTC  431
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lcl|Query_47323
Uncultured bacterium partial 16S rRNA gene, isolate Be20
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: XZX-139
Bacillus anthracis strain 1-Sj-5-2-3-M 16S ribosomal RNA gene, partial sequence
Bacillus sp. RO1S-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. BBAR-01d 16S ribosomal RNA gene, partial sequence
Bacillus sp. QY1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain EM13 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain JC80 16S ribosomal RNA gene, partial sequence
Bacillus sp. XM1 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, isolate BCs1
Bacillus sp. DSN53 gene for 16S rRNA, partial sequence
Bacillus sp. Y04 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate BF0001D030
Bacillus sp. ES2-45 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus thuringiensis strain RB90 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb39(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. VOC11 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb55 16S ribosomal RNA gene, partial sequence
Bacterium C0528 16S ribosomal RNA gene, partial sequence
Bacillus sp. I4X 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NM2E11 16S ribosomal RNA gene, partial sequence
Bacillus sp. FGG1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_19 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_32 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4641 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain P1 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain IHB B 7117 16S ribosomal RNA gene, partial sequence
Bacillus sp. N5/665 partial 16S rRNA gene, strain N5/665
Uncultured bacterium partial 16S rRNA gene, isolate Br2
Uncultured bacterium partial 16S rRNA gene, isolate Be21
Bacillus sp. EM7 16S rRNA gene, isolate EM7
Bacillus anthracis 16S rRNA gene, isolate EM36
Bacillus sp. ADI1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PVR-YHB-1-1 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain BHR1P2B2 16S ribosomal RNA gene, partial sequence
Bacillus sp. BS24 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain FJM2 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: QX-54
Bacillus sp. DB14344 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14692 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: QX-85
Bacillus thuringiensis strain FJM3 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 5A 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain BS1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain JMG-03 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain GZDF1 16S ribosomal RNA gene, partial sequence
Bacillus sp. WM64 16S rRNA gene, isolate WM64
Bacillus anthracis 16S rRNA gene, isolate EM11
Bacillus sp. SF2-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Be3
Bacillus cereus strain LP10_S10 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain IHB B 7196 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 7021 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain HD567 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_38 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_22 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis serovar galleriae strain HD-29, complete genome
Bacillus sp. B1(2015) 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 18033 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RHDTWG188 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RHDTWG185 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone RHDTWG181 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C6A08 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C6A22 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C5B09-1 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone C3D04 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4516D 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4312S 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain DC2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Br34
firmicutes | 2 leaves
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, isolate: LZX-54
Bacillus cereus strain FJM4 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 11B 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain BS14 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MHS 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NXUGDS005 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain K2-1 16S ribosomal RNA gene, partial sequence
Bacillus sp. EM25b 16S rRNA gene, isolate EM25b
Bacillus sp. JBS-28 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Be6
Bacillus cereus strain KG5 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain IHB B 7206 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain IHB B 7070 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain HD867 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_40 16S ribosomal RNA gene, partial sequence
Bacillus sp. gx13 16S ribosomal RNA gene, partial sequence
Bacillus sp. enrichment culture clone S16 16S ribosomal RNA gene, partial sequence
Bacillus sp. CMAP11 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Unidentified bacterium clone MEB002 16S ribosomal RNA gene, partial sequence
Bacillus sp. SMF5 partial 16S rRNA gene
Uncultured prokaryote clone seq_M-L8_16SR 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4109M 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14882 16S ribosomal RNA gene, partial sequence
0.001

5- The phylogenetic analysis of bacteria isolated from lift buttons samples

Staphylococcus warneri BCL-34

Staphylococcus warneri strain MBS022 16S ribosomal RNA gene, partial sequence

Sequence ID: KT582294.1 **Length:** 1486 **Number of Matches:** 1

Range 1: 820 to 1424 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1077 bits(583)	0.0	599/606(99%)	3/606(0%)	Plus/Minus

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Query  19    TAAATGGTTACTCCACCGGCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTG  78
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Sbjct  1424  TAAATGGTTACTCCACCGGCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTG  1365

Query  79    TACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTACGATTACTAGCGATTCCAG  138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1364  TACAAGACCCGGGAACGTATTCACCGTAGCATGCTGATCTACGATTACTAGCGATTCCAG  1305

Query  139   CTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTTTATGGGATTTGCT  198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1304  CTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAACAACTTTATGGGATTTGCT  1245

Query  199   TGACCTCGCGGTTTAGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAGCCCAAATC  258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1244  TGACCTCGCGGTTTAGCTGCCCTTTGTATTGTCCATTGTAGCACGTGTGTAGCCCAAATC  1185

Query  259   ATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCA  318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1184  ATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCA  1125

Query  319   ACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGAC  378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1124  ACTTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGCGCTCGTTGCGGGAC  1065

Query  379   TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCC  438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1064  TTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCC  1005

Query  439   CCCGAAGGGGAAGACTCTATCTCTAGAGCGGTCAAAGGATGTCAAGATTTGGTAAGGTTC  498
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1004  CCCGAAGGGGAAGACTCTATCTCTAGAGCGGTCAAAGGATGTCAAGATTTGGTAAGGTTC  945

Query  499   TTCGCGTTGCTTCAAATTAAACCACATGCTCCACCGTTGGTGCGG--CCCCGTCAATTCT  556
             |||||||||||||||||||||||||||||||||||| | ||||||  ||||||||||||
Sbjct  944   TTCGCGTTGCTTCAAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTCAATTCC  885

Query  557   TTTGATTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTAGCTGCA  616
             ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  884   TTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTT-AGCTGCA  826

Query  617   GCACTA  622
             ||||||
Sbjct  825   GCACTA  820
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firmicutes | 2 leaves
Staphylococcus warneri strain MBS022 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain MBS011 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain CPI 2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. ChDC B392 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. ChDC B393 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. PSB-18 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. PSB-21 16S ribosomal RNA gene, partial sequence
Psychrobacter pulmonis strain SL-9 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. DF6n-C small subunit ribosomal RNA gene, partial sequence
Staphylococcus pasteuri partial 16S rRNA gene, isolate OCAT1
Staphylococcus warneri partial 16S rRNA gene, isolate OCAT2
Staphylococcus warneri partial 16S rRNA gene, isolate OCAT9
Staphylococcus sp. OCAT11 partial 16S rRNA gene, isolate OCAT11
Staphylococcus warneri partial 16S rRNA gene, isolate OCAT13
Staphylococcus sp. OCAT14 partial 16S rRNA gene, isolate OCAT14
Staphylococcus warneri partial 16S rRNA gene, isolate OCAT15
Staphylococcus warneri partial 16S rRNA gene, isolate OCAT20
Staphylococcus warneri partial 16S rRNA gene, isolate OCOB3
Staphylococcus warneri partial 16S rRNA gene, isolate OCOB8
Uncultured Staphylococcus sp. clone JU-EB2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain JU-SB2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain MRS-2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. DVRSG-2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain LH-T2 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain YZ-T1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. NBM-83 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain 81b 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain MJMG7.13 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. P34 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Bts 21b partial 16S rRNA gene, isolate Bts 21b
Staphylococcus warneri strain STP02 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. enrichment culture clone zhuowei 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain RJ24 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain CS.B10 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain MAL_1A 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri strain MGH119 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CE3E4 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CE3E5 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CE3E1 16S ribosomal RNA gene, partial sequence
Staphylococcus pasteuri strain KG-63 16S ribosomal RNA gene, partial sequence
Staphylococcus warneri gene for 16S ribosomal RNA, partial sequence, strain: SH13
Staphylococcus warneri strain 1058 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. s71S1a 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone M21P1FI0 16S ribosomal RNA gene, partial sequence
firmicutes | 55 leaves
0.0004

Micrococcus luteus MBS022

Micrococcus luteus strain BCL-34 16S ribosomal RNA gene, partial sequence

Sequence ID: KM378607.1 Length: 1394 Number of Matches: 1

Range 1: 1 to 1393 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
2560 bits(1386)	0.0	1391/1393(99%)	1/1393(0%)	Plus/Plus

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Query  1     TGC-AGTCGAACGATGAAGCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGTAAC  59
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGCAAGTCGAACGATGAAGCCCAGCTTGCTGGGTGGATTAGTGGCGAACGGGTGAGTAAC  60

Query  60    ACGTGAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCTAATACCGGAT  119
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Sbjct  61    ACGTGAGTAACCTGCCCTTAACTCTGGGATAAGCCTGGGAAACTGGGTCTAATACCGGAT  120

Query  120   AGGAGCGCCGACCGCATGGTGGGTGTTGGAAAGATTTATCGGTTTTGGATGGACTCGCGG  179
             |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AGGAGCGCCTACCGCATGGTGGGTGTTGGAAAGATTTATCGGTTTTGGATGGACTCGCGG  180

Query  180   CCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAG  239
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Sbjct  181   CCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAG  240

Query  240   AGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTG  299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTG  300

Query  300   GGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCC  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCC  360

Query  360   TTCGGGTTGTAAACCTCTTTCAGTAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAA  419
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Sbjct  361   TTCGGGTTGTAAACCTCTTTCAGTAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAA  420

Query  420   GCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCCGGA  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GCACCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTATCCGGA  480

Query  480   ATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTCGTGAAAGTCCGGGGCT  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGTCGTGAAAGTCCGGGGCT  540

Query  540   TAACCCCGGATCTGCGGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTC  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TAACCCCGGATCTGCGGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTC  600

Query  600   CTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTC  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTC  660

Query  660   TGGGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGATTAGATACCCTG  719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TGGGCTGTAACTGACGCTGAGGAGCGAAAGCATGGGGAGCGAACAGGATTAGATACCCTG  720

Query  720   GTAGTCCATGCCGTAAACGTTGGGCACTAGGTGTGGGGACCATTCCACGGTTTCCGCGCC  779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   GTAGTCCATGCCGTAAACGTTGGGCACTAGGTGTGGGGACCATTCCACGGTTTCCGCGCC  780

Query  780   GCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGG  839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   GCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGG  840

Query  840   AATTGACGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAACGCGAAGA  899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   AATTGACGGGGGCCCGCACAAGCGGCGGAGCATGCGGATTAATTCGATGCAACGCGAAGA  900

Query  900   ACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGAGATACGGTTTCCCCTTTGGGGC  959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   ACCTTACCAAGGCTTGACATGTTCTCGATCGCCGTAGAGATACGGTTTCCCCTTTGGGGC  960

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Sbjct  961   GGGTTCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC  1020

Query  1020  CGCAACGAGCGCAACCCTCGTTCCATGTTGCCAGCACGTAATGGTGGGGACTCATGGGAG  1079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021  CGCAACGAGCGCAACCCTCGTTCCATGTTGCCAGCACGTAATGGTGGGGACTCATGGGAG  1080

Query  1080  ACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAATCATCATGCCCCTTATGT  1139
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Sbjct  1081  ACTGCCGGGGTCAACTCGGAGGAAGGTGAGGACGACGTCAAATCATCATGCCCCTTATGT  1140

Query  1140  CTTGGGCTTCACGCATGCTACAATGGCCGGTACAATGGGTTGCGATACTGTGAGGTGGAG  1199
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Query  1200  CTAATCCCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC  1259
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Sbjct  1201  CTAATCCCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTC  1260

Query  1260  GGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTAC  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261  GGAGTCGCTAGTAATCGCAGATCAGCAACGCTGCGGTGAATACGTTCCCGGGCCTTGTAC  1320

Query  1320  ACACCGCCCGTCAAGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCTAACCCTTGTG  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  ACACCGCCCGTCAAGTCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCTAACCCTTGTG  1380

Query  1380  GGGGAGCCGTCGA  1392
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Sbjct  1381  GGGGAGCCGTCGA  1393
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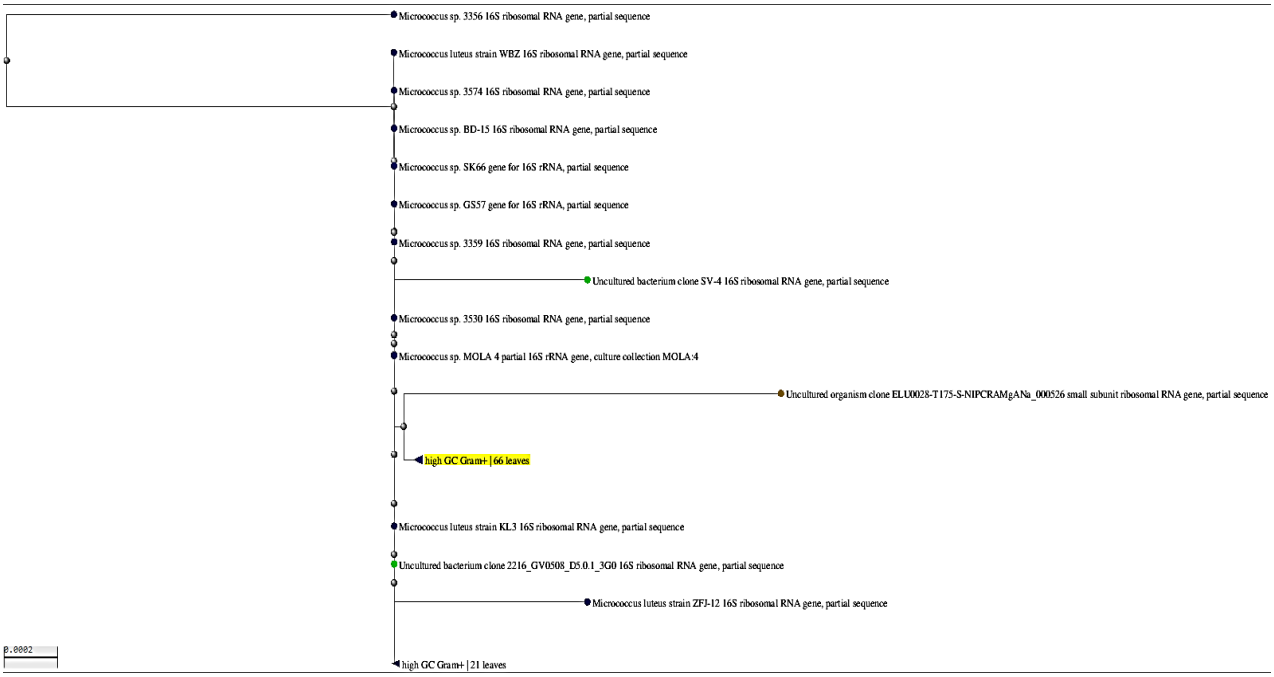
Micrococcus sp. 3356 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain WBZ 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3574 16S ribosomal RNA gene, partial sequence
Micrococcus sp. BD-15 16S ribosomal RNA gene, partial sequence
Micrococcus sp. SK66 gene for 16S rRNA, partial sequence
Micrococcus sp. GS57 gene for 16S rRNA, partial sequence
Micrococcus sp. 3359 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone SV-4 16S ribosomal RNA gene, partial sequence
Micrococcus sp. 3530 16S ribosomal RNA gene, partial sequence
Micrococcus sp. MOLA 4 partial 16S rRNA gene, culture collection MOLA:4
Uncultured organism clone ELU0028-T175-S-NIPCRAMgANa_000526 small subunit ribosomal RNA gene, partial sequence
high GC Gram+ | 66 leaves
Micrococcus luteus strain KL3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2216_GV0508_D5.0.1_3G0 16S ribosomal RNA gene, partial sequence
Micrococcus luteus strain ZFJ-12 16S ribosomal RNA gene, partial sequence
0.0002
high GC Gram+ | 21 leaves

Staphylococcus epidermidis

Staphylococcus epidermidis partial 16S rRNA gene, strain BGHMC5

Sequence ID: FR797804.1 **Length:** 815 **Number of Matches:** 1

Range 1: 1 to 815 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1506 bits(815)	0.0	815/815(100%)	0/815(0%)	Plus/Plus

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Query  1    AGAAAGTGGAATCCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGG  60
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Sbjct  1    AGAAAGTGGAATCCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGG  60

Query  61   CGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAG  120

Query  121  GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCC  180

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Sbjct  181  GCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGT  240

Query  241  TGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGA  300

Query  301  AGCAACGCGAAGAACCTTACCAAATCTTGACATCCTCTGACCCCTCTAGAGATAGAGTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCAACGCGAAGAACCTTACCAAATCTTGACATCCTCTGACCCCTCTAGAGATAGAGTTT  360

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Sbjct  421  TGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCATTAAGTTGG  480

Query  481  GCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC  540
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Sbjct  481  GCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC  540

Query  541  ATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAA  600
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Sbjct  541  ATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAA  600

Query  601  CCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCG  660
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Sbjct  601  CCGCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCG  660

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  ACTATATGAAGCTGGAATCGCTAGTAATCGTAGATCAGCATGCTACGGTGAATACGTTCC  720

Query  721  CGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  CGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGA  780

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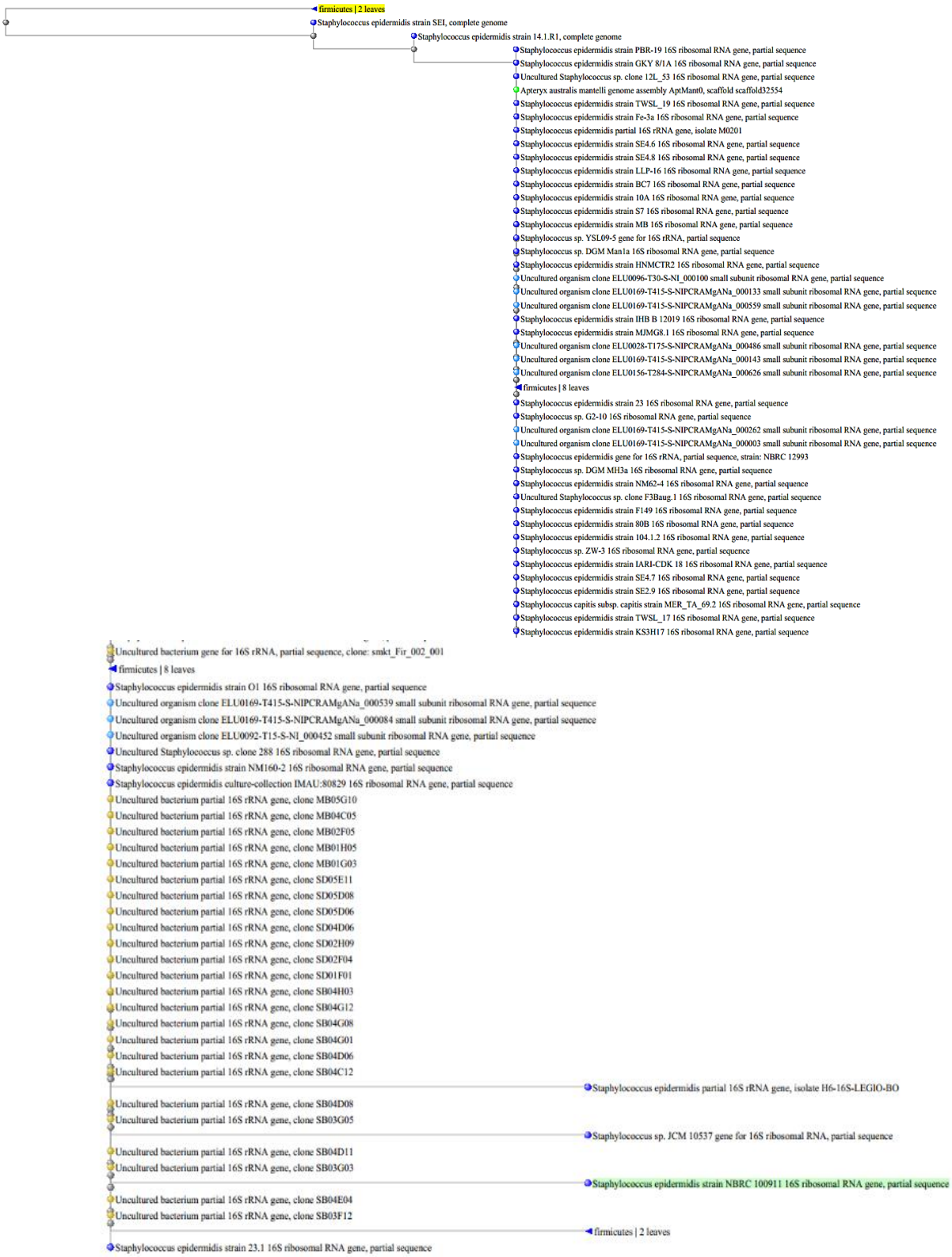
firmicutes | 2 leaves
Staphylococcus epidermidis strain SEI, complete genome
Staphylococcus epidermidis strain 14.1.R1, complete genome
Staphylococcus epidermidis strain PBR-19 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain GKY 8/1A 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone 12L_53 16S ribosomal RNA gene, partial sequence
Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold32554
Staphylococcus epidermidis strain TWSL_19 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain Fe-3a 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis partial 16S rRNA gene, isolate M0201
Staphylococcus epidermidis strain SE4.6 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain SE4.8 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain LLP-16 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain BC7 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 10A 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain S7 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain MB 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. YSL09-5 gene for 16S rRNA, partial sequence
Staphylococcus sp. DGM Man1a 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain HNMCTR2 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0096-T30-S-NI_000100 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000133 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000559 small subunit ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain IHB B 12019 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain MJMG8.1 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0028-T175-S-NIPCRAMgANa_000486 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000143 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0156-T284-S-NIPCRAMgANa_000626 small subunit ribosomal RNA gene, partial sequence
firmicutes | 8 leaves
Staphylococcus epidermidis strain 23 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. G2-10 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000262 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000003 small subunit ribosomal RNA gene, partial sequence
Staphylococcus epidermidis gene for 16S rRNA, partial sequence, strain: NBRC 12993
Staphylococcus sp. DGM MH3a 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain NM62-4 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone F3Baug.1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain F149 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 80B 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 104.1.2 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. ZW-3 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain IARI-CDK 18 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain SE4.7 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain SE2.9 16S ribosomal RNA gene, partial sequence
Staphylococcus capitis subsp. capitis strain MER_TA_69.2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain TWSL_17 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain KS3H17 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: smkt_Fir_002_001
firmicutes | 8 leaves
Staphylococcus epidermidis strain O1 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000539 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0169-T415-S-NIPCRAMgANa_000084 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0092-T15-S-NI_000452 small subunit ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone 288 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain NM160-2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis culture-collection IMAU:80829 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone MB05G10
Uncultured bacterium partial 16S rRNA gene, clone MB04C05
Uncultured bacterium partial 16S rRNA gene, clone MB02F05
Uncultured bacterium partial 16S rRNA gene, clone MB01H05
Uncultured bacterium partial 16S rRNA gene, clone MB01G03
Uncultured bacterium partial 16S rRNA gene, clone SD05E11
Uncultured bacterium partial 16S rRNA gene, clone SD05D08
Uncultured bacterium partial 16S rRNA gene, clone SD05D06
Uncultured bacterium partial 16S rRNA gene, clone SD04D06
Uncultured bacterium partial 16S rRNA gene, clone SD02H09
Uncultured bacterium partial 16S rRNA gene, clone SD02F04
Uncultured bacterium partial 16S rRNA gene, clone SD01F01
Uncultured bacterium partial 16S rRNA gene, clone SB04H03
Uncultured bacterium partial 16S rRNA gene, clone SB04G12
Uncultured bacterium partial 16S rRNA gene, clone SB04G08
Uncultured bacterium partial 16S rRNA gene, clone SB04G01
Uncultured bacterium partial 16S rRNA gene, clone SB04D06
Uncultured bacterium partial 16S rRNA gene, clone SB04C12
Staphylococcus epidermidis partial 16S rRNA gene, isolate H6-16S-LEGIO-BO
Uncultured bacterium partial 16S rRNA gene, clone SB04D08
Uncultured bacterium partial 16S rRNA gene, clone SB03G05
Staphylococcus sp. JCM 10537 gene for 16S ribosomal RNA, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SB04D11
Uncultured bacterium partial 16S rRNA gene, clone SB03G03
Staphylococcus epidermidis strain NBRC 100911 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SB04E04
Uncultured bacterium partial 16S rRNA gene, clone SB03F12
firmicutes | 2 leaves
Staphylococcus epidermidis strain 23.1 16S ribosomal RNA gene, partial sequence

6 - The phylogenetic analysis of bacteria isolated from vacuum cleaner dust samples

Bacillus thuringiensis FJ174596.1

Bacillus thuringiensis strain 104XG46 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|FJ174596.1| **Length:** 1049 **Number of Matches:** 1

Range 1: 59 to 1018 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1651 bits(1830)	0.0	944/960(98%)	3/960(0%)	Plus/Plus

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Query  1     AGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGG  60
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Sbjct  59    AGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGGG  118

Query  61    AAACCGGGGCTAATACCGGATAATATTTTGAACTGCATGGTTCGAAATTGAAAGGCGGCT  120
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Sbjct  119   AAACCGGGGCTAATACCGGATAACATTTTGAACTGCATGGTTCGAAATTGAAAGGCGGCT  178

Query  121   TCGGCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCA  180
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Sbjct  179   TCGGCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCA  238

Query  181   CCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC  240
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Sbjct  239   CCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACAC  298

Query  241   GGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGAC  300
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Sbjct  299   GGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGAC  358

Query  301   GGAGCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAG  360
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Sbjct  359   GGAGCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAAG  418

Query  361   AACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTA  420
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Sbjct  419   AACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTA  478

Query  421   ACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGC  480
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Sbjct  479   ACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGC  538

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Sbjct  539   GTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGA  598
Query  541   GGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGC  600
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Query  721   CCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGC  780
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Sbjct  779   CCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGC  838

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Sbjct  839   ATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAGGAATTGACGGGGG  898

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Sbjct  899   CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAGAACCTTACCAGGTC  958

Query  899   TTGACTTCCTCTGAAACCCTANAAATAGGGCTTC-CCTTCGGGAACAAAAGGACAggggg  957
             ||||| |||||||||||||| | |||||||||| ||||||||| || |  |||||| ||
Sbjct  959   TTGACATCCTCTGAAACCCTAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAGGTGG  1018
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Bacillus thuringiensis clone C05 16S ribosomal RNA gene, partial sequence
lcl|Query_55687
Bacillus cereus 16S ribosomal RNA gene, partial sequence
Bacillus sp. ST21 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
firmicutes | 7 leaves
firmicutes | 2 leaves
Bacillus toyonensis strain AEMREG6 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus thuringiensis strain HS18-1, complete genome
firmicutes | 2 leaves
Bacillus sp. H434 16S ribosomal RNA gene, partial sequence
Bacterium NR14 16S ribosomal RNA gene, partial sequence
Bacterium NF8 16S ribosomal RNA gene, partial sequence
Bacterium NF6 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4052G 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4516D 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_34 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_41 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_69 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Am_75 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_Ne_54 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_25 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_31 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 5_St_43 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain LS-8 16S ribosomal RNA gene, partial sequence
Bacillus anthracis strain IHB B 15784 16S ribosomal RNA gene, partial sequence
Bacillus sp. FGG1 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain KNUSC3015 16S ribosomal RNA gene, partial sequence
Bacillus sp. Hin7.3 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain K206 16S ribosomal RNA gene, partial sequence
Bacillus sp. NSH-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. CC6G 16S ribosomal RNA gene, partial sequence
Bacillus toyonensis strain 26S.2 16S ribosomal RNA gene, partial sequence
Bacillus toyonensis strain 26S.1 16S ribosomal RNA gene, partial sequence
Bacillus toyonensis strain 26K.2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NCIM 2155 16S ribosomal RNA gene, partial sequence
Bacillus sp. 3HH-8 16S ribosomal RNA gene, partial sequence
Bacterium YTM085716 from China 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain IHB B 10262 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis 16S ribosomal RNA gene, partial sequence
Bacillus sp. TPFDDF-15001 16S ribosomal RNA gene, partial sequence
Bacillus sp. TPFDDF-15002 16S ribosomal RNA gene, partial sequence
Bacillus sp. TPFDDF-15003 16S ribosomal RNA gene, partial sequence
Bacillus anthracis partial 16S rRNA gene, isolate BD17-S12
Bacillus sp. TPFDDF-15004 16S ribosomal RNA gene, partial sequence
Bacillus sp. TPFDDF-15005 16S ribosomal RNA gene, partial sequence
Bacillus sp. TPFDDF-15006 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain X022 16S ribosomal RNA gene, partial sequence
Bacillus sp. POUC 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain R12 16S ribosomal RNA gene, partial sequence
Bacillus sp. R12(2014) 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain YB18 16S ribosomal RNA gene, partial sequence
Bacillus sp. enrichment culture clone PRGSd-MS-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14692 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain FJM4 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain FJM3 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain FJM2 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain JMG-03 16S ribosomal RNA gene, partial sequence
Bacillus sp. B42(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. B37(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. TD6#11 16S ribosomal RNA gene, partial sequence
Bacillus mycoides strain YR7 16S ribosomal RNA gene, partial sequence
Bacillus cereus gene for 16S ribosomal RNA, partial sequence, strain: NRKT
Bacillus cereus strain NXUGDS005 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain 6N 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain DL10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Be6
Bacillus sp. N5/665 partial 16S rRNA gene, strain N5/665
Bacillus thuringiensis strain IHB B 7070 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain P1 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain HD867 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_38 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PT_19 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
firmicutes | 4 leaves
0.0009
0.0009

Bacillus mycoides **KR088435.1**

Bacillus mycoides strain St02 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KR088435.1| **Length:** 1398 **Number of Matches:** 1

Range 1: 396 to 1367 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1703 bits(1888)	0.0	964/973(99%)	3/973(0%)	Plus/Minus

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Query  1     TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1367  TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTG  1308

Query  61    ATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1307  ATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACT  1248

Query  121   GAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1247  GAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCGTCCAT  1188

Query  181   TGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT  240
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Sbjct  1187  TGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT  1128

Query  241   CCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACTAAGAT  300
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Sbjct  1127  CCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACTAAGAT  1068

Query  301   CAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC  360
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Sbjct  1067  CAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC  1008

Query  361   CATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTTGTCAGAGG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1007  CATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTTGTCAGAGG  948

Query  421   ATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  947   ATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCT  888

Query  481   TGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGA  540
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Sbjct  887   TGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAGGCGGA  828

Query  541   GTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCAT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  827   GTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCAT  768

Query  601   CGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCGCCT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  767   CGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCGCCT  708

Query  661   CAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTACG  720
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Sbjct  707   CAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCTCTACG  648

Query  721   CATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCAGTTTC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  647   CATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCAGTTTC  588

Query  781   CAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAAACTTAAAAAACCACCTGCGC  840
             |||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||
Sbjct  587   CAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACCTGCGC  528

Query  841   GCGCTTTACGCCCAATAATTCCGGA-AACGCTTGCCACCTACGTATTACCGCGGCTGCTG  899
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  527   GCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTG  468

Query  900   GCACGTAATTAGCCG-GGCTTTCTGGGTTAGGTACCGTCAAGGGGCCAGCTTATTCAACT  958
             ||||||| ||||||| |||||||| |||||||||||||||||| ||||||||||||||||
Sbjct  467   GCACGTAGTTAGCCGTGGCTTTCT-GGTTAGGTACCGTCAAGGTGCCAGCTTATTCAACT  409

Query  959   AACCCTTGTTCTT  971
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Sbjct  408   AGCACTTGTTCTT  396
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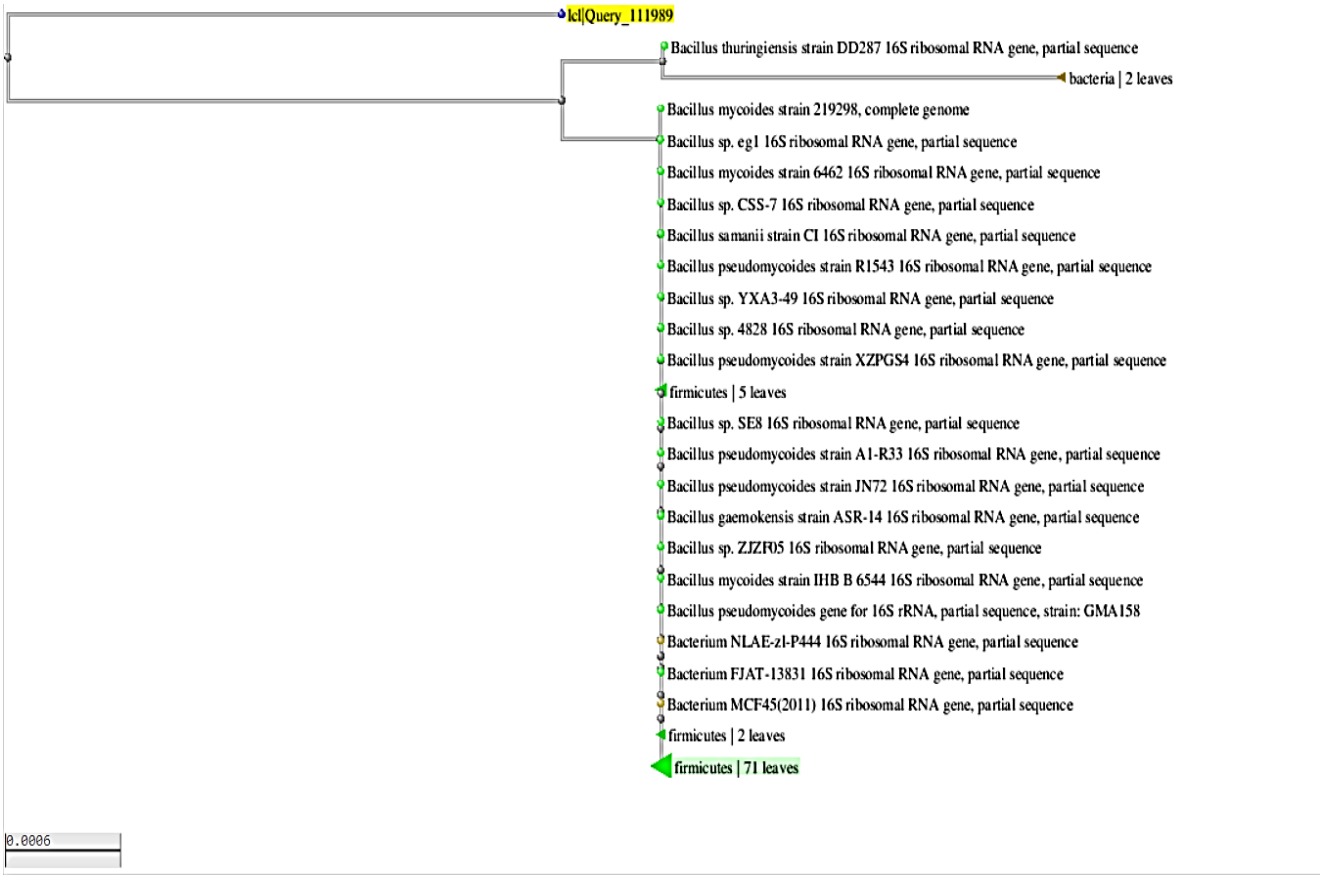
lcl|Query_111989
Bacillus thuringiensis strain DD287 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Bacillus mycoides strain 219298, complete genome
Bacillus sp. eg1 16S ribosomal RNA gene, partial sequence
Bacillus mycoides strain 6462 16S ribosomal RNA gene, partial sequence
Bacillus sp. CSS-7 16S ribosomal RNA gene, partial sequence
Bacillus samanii strain CI 16S ribosomal RNA gene, partial sequence
Bacillus pseudomycoides strain R1543 16S ribosomal RNA gene, partial sequence
Bacillus sp. YXA3-49 16S ribosomal RNA gene, partial sequence
Bacillus sp. 4828 16S ribosomal RNA gene, partial sequence
Bacillus pseudomycoides strain XZPGS4 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus sp. SE8 16S ribosomal RNA gene, partial sequence
Bacillus pseudomycoides strain A1-R33 16S ribosomal RNA gene, partial sequence
Bacillus pseudomycoides strain JN72 16S ribosomal RNA gene, partial sequence
Bacillus gaemokensis strain ASR-14 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZJZF05 16S ribosomal RNA gene, partial sequence
Bacillus mycoides strain IHB B 6544 16S ribosomal RNA gene, partial sequence
Bacillus pseudomycoides gene for 16S rRNA, partial sequence, strain: GMA158
Bacterium NLAE-zl-P444 16S ribosomal RNA gene, partial sequence
Bacterium FJAT-13831 16S ribosomal RNA gene, partial sequence
Bacterium MCF45(2011) 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 71 leaves
0.0006

Bacillus licheniformis DQ071560.1

Bacillus licheniformis strain MKU 1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|DQ071560.1| **Length:** 1430 **Number of Matches:** 1

Range 1: 425 to 1393 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1694 bits(1878)	0.0	957/969(99%)	0/969(0%)	Plus/Minus

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Query  1     TTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCG  60
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Sbjct  1393  TTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCG  1334

Query  61    GCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1333  GCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGA  1274

Query  121   TCCGAACTGAGAACAGATTTGTGGGATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTT  180
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Sbjct  1273  TCCGAACTGAGAACAGATTTGTGGGATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTT  1214

Query  181   CTGCCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC  240
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Sbjct  1213  CTGCCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC  1154

Query  241   CCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCA  300
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Sbjct  1153  CCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCA  1094

Query  301   ACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTG  360
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Sbjct  1093  ACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTG  1034

Query  361   ACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTT  420
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Sbjct  1033  ACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTT  974

Query  421   GTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  973   GTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCT  914

Query  481   CCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  913   CCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCC  854

Query  541   CAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTAAAGGGCGGAAACCCTCTAACACTTA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  853   CAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTAAAGGGCGGAAACCCTCTAACACTTA  794

Query  601   GCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTT  660
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Sbjct  793   GCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTT  734

Query  661   TCGCGCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACA  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  733   TCGCGCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACA  674

Query  721   TCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  673   TCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCC  614

Query  781   CCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  613   CCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACC  554

Query  841   GCCTGCGCGCGCTTTACCCCCAATAATTCCCGGAAACCCTTGCCACCTACGTATTACCGC  900
             |||||||||||||||| |||||||||||  | ||| ||||||||||||||||||||||||
Sbjct  553   GCCTGCGCGCGCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGC  494

Query  901   GGCTGCTGGGACGTAATTAGCCGGGGCTTTCTGGTTAGGTACCGTCAAGGAACCCCCCTA  960
             |||||||||  |||||  |||||||  |||||||||||||||||||||||||  |||  |||||
Sbjct  493   GGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTACCGCCCTA  434

Query  961   TTCAAAAGG  969
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Sbjct  433   TTCGAACGG  425
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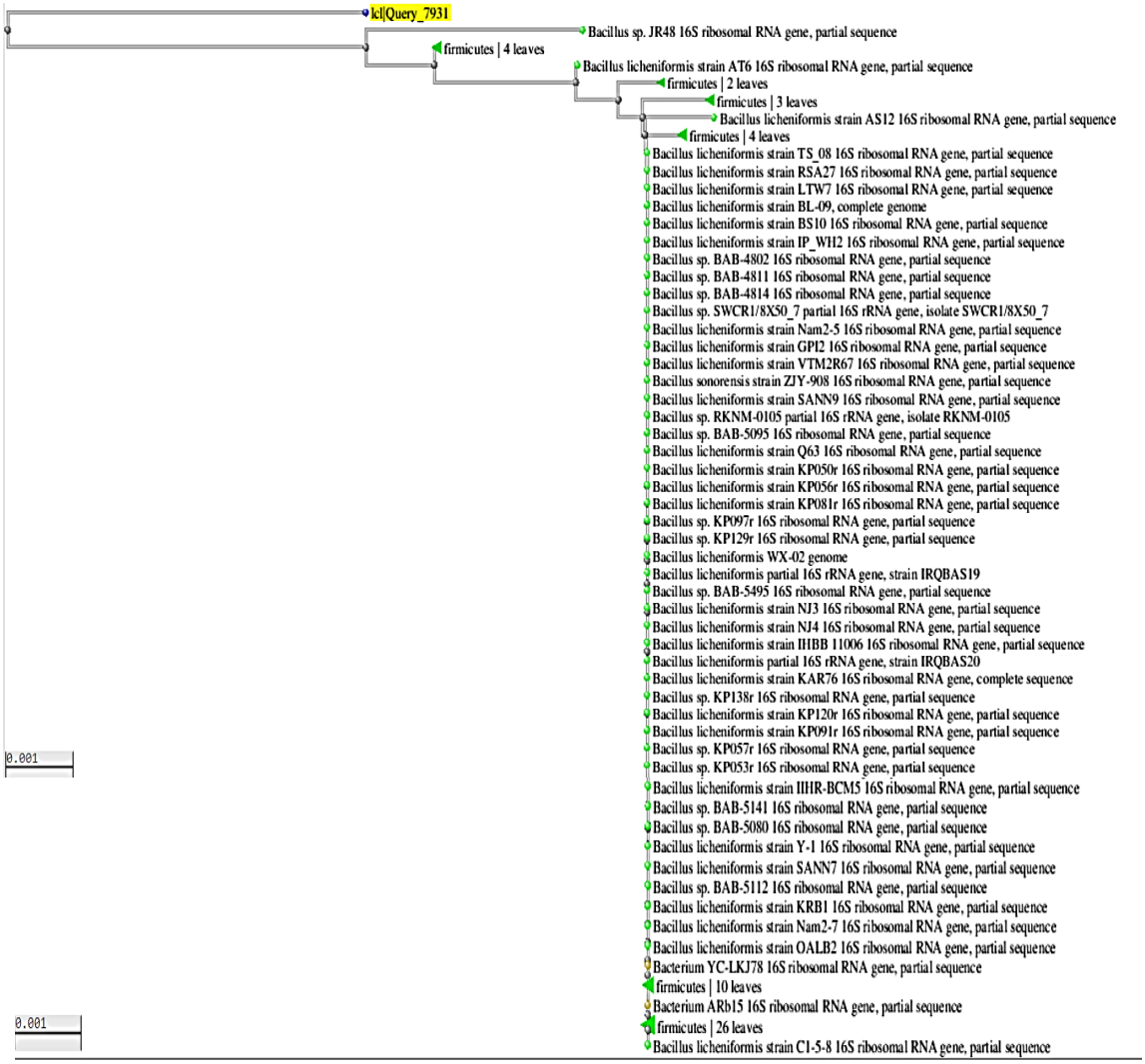
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Bacillus sp. JR48 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Bacillus licheniformis strain AT6 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 3 leaves
Bacillus licheniformis strain AS12 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Bacillus licheniformis strain TS_08 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain RSA27 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain LTW7 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain BL-09, complete genome
Bacillus licheniformis strain BS10 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain IP_WH2 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4802 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4811 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4814 16S ribosomal RNA gene, partial sequence
Bacillus sp. SWCR1/8X50_7 partial 16S rRNA gene, isolate SWCR1/8X50_7
Bacillus licheniformis strain Nam2-5 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain GPI2 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain VTM2R67 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain ZJY-908 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SANN9 16S ribosomal RNA gene, partial sequence
Bacillus sp. RKNM-0105 partial 16S rRNA gene, isolate RKNM-0105
Bacillus sp. BAB-5095 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Q63 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP050r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP056r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP081r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP097r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP129r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis WX-02 genome
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS19
Bacillus sp. BAB-5495 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NJ3 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NJ4 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain IHBB 11006 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS20
Bacillus licheniformis strain KAR76 16S ribosomal RNA gene, complete sequence
Bacillus sp. KP138r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP120r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP091r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP057r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP053r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain IIHR-BCM5 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5141 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5080 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Y-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SANN7 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5112 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KRB1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Nam2-7 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain OALB2 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ78 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
Bacterium ARb15 16S ribosomal RNA gene, partial sequence
firmicutes | 26 leaves
Bacillus licheniformis strain C1-5-8 16S ribosomal RNA gene, partial sequence
0.001
0.001

Bacillus subtilis KF220577.1

Bacillus subtilis strain YLB-P1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF220577.1| **Length:** 1050 **Number of Matches:** 1

Range 1: 51 to 1025 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1653 bits(1832)	0.0	955/975(98%)	5/975(0%)	Plus/Plus

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Query  1     CTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATA  60
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Sbjct  51    CTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATA  110

Query  61    ACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACATAAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  111   ACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAACATAAA  170

Query  121   AGGTGGCTTYGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTA  180
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171   AGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTA  230

Query  181   ACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231   ACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  290

Query  241   TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAA  300
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Sbjct  291   TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAA  350

Query  301   AGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  360
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Sbjct  351   AGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  410

Query  361   TAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGC  420
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Sbjct  411   TAGGGAAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGC  470

Query  421   CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  480
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Sbjct  471   CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  530

Query  481   TATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCA  540
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Sbjct  531   TATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCA  590

Query  541   ACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCA  600
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Sbjct  591   ACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCA  650

Query  601   CGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTG  660
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Query  661   GTCTGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGT  720
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Query  721   AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCA  780
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Sbjct  771   AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCA  830

Query  781   GCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAAT  840
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Sbjct  831   GCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAAT  890

Query  841   TCACGGGGGCCCGCACAAGCGGGGGAGCATGTGATTT-ATTCGAAGC-ACGCGAAAACCT  898
             | |||||||||||||||||||| |||||||||| ||| ||||||||| ||||||| ||||
Sbjct  891   TGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGACCT  950

Query  899   TACCA-GTCTTGACTTCCTCTGAGATCCTaaaaaaaGGACGTCCCCTTC-GGGCAAAAGG  956
             ||||| |||||||| |||||||| |||||| | | |||||||||||||| |||| ||  |
Sbjct  951   TACCAGGTCTTGACATCCTCTGACATCCTAGAGATAGGACGTCCCCTTCGGGGCCAAGTG  1010

Query  957   ACAG-GGGGGATGGT  970
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Sbjct  1011  ACAGTGGTGCATGGT  1025
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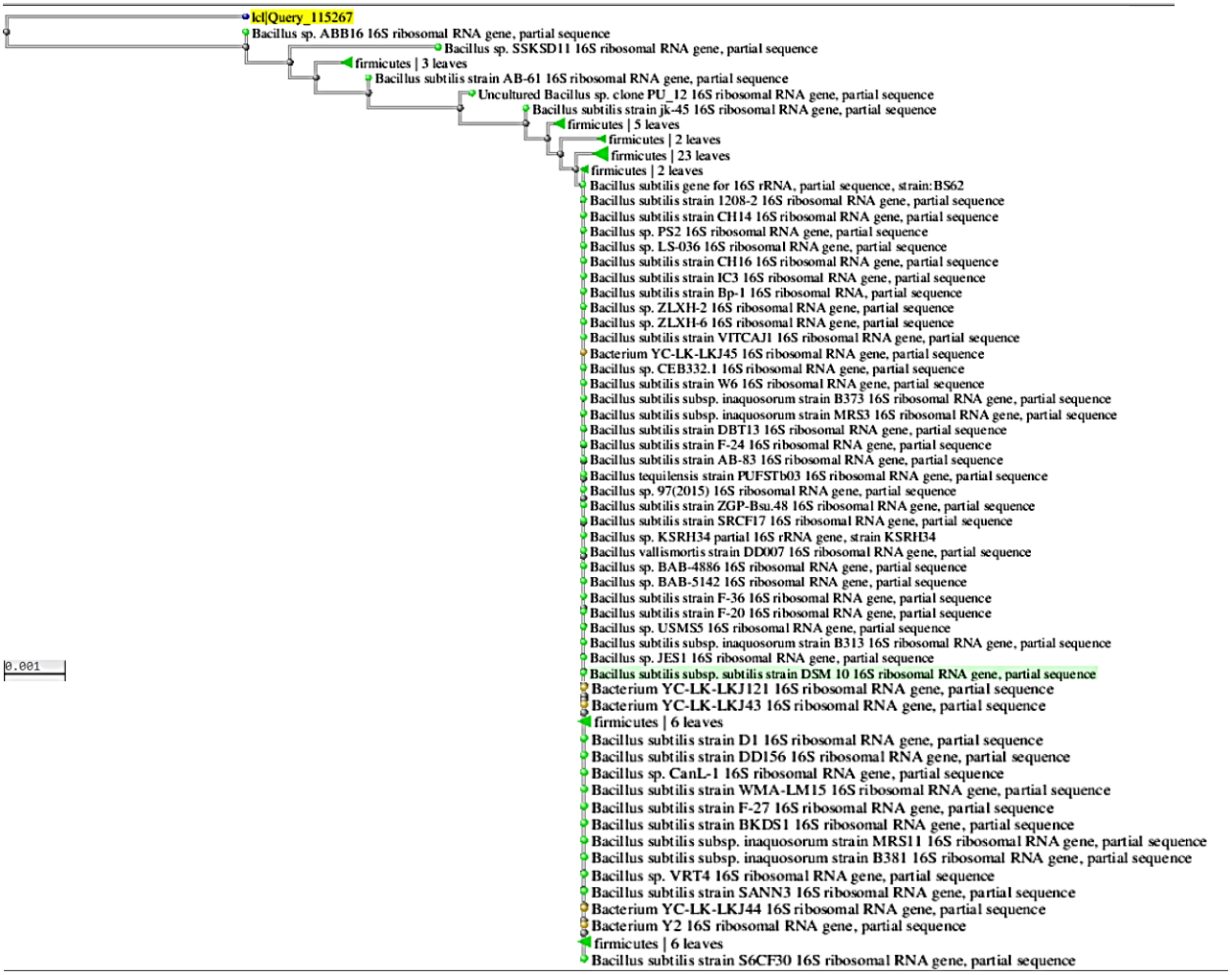
lcl|Query_115267
Bacillus sp. ABB16 16S ribosomal RNA gene, partial sequence
Bacillus sp. SSKSD11 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Bacillus subtilis strain AB-61 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone PU_12 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain jk-45 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
firmicutes | 2 leaves
firmicutes | 23 leaves
firmicutes | 2 leaves
Bacillus subtilis gene for 16S rRNA, partial sequence, strain:BS62
Bacillus subtilis strain 1208-2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain CH14 16S ribosomal RNA gene, partial sequence
Bacillus sp. PS2 16S ribosomal RNA gene, partial sequence
Bacillus sp. LS-036 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain CH16 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain IC3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Bp-1 16S ribosomal RNA, partial sequence
Bacillus sp. ZLXH-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-6 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain VITCAJ1 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ45 16S ribosomal RNA gene, partial sequence
Bacillus sp. CEB332.1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain W6 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain B373 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain MRS3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DBT13 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain F-24 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain AB-83 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis strain PUFSTb03 16S ribosomal RNA gene, partial sequence
Bacillus sp. 97(2015) 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain ZGP-Bsu.48 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SRCF17 16S ribosomal RNA gene, partial sequence
Bacillus sp. KSRH34 partial 16S rRNA gene, strain KSRH34
Bacillus vallismortis strain DD007 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4886 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5142 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain F-36 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain F-20 16S ribosomal RNA gene, partial sequence
Bacillus sp. USMS5 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain B313 16S ribosomal RNA gene, partial sequence
Bacillus sp. JES1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ121 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ43 16S ribosomal RNA gene, partial sequence
firmicutes | 6 leaves
Bacillus subtilis strain D1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DD156 16S ribosomal RNA gene, partial sequence
Bacillus sp. CanL-1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain WMA-LM15 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain F-27 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain BKDS1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain MRS11 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain B381 16S ribosomal RNA gene, partial sequence
Bacillus sp. VRT4 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SANN3 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ44 16S ribosomal RNA gene, partial sequence
Bacterium Y2 16S ribosomal RNA gene, partial sequence
firmicutes | 6 leaves
Bacillus subtilis strain S6CF30 16S ribosomal RNA gene, partial sequence
0.001

7-The phylogenetic analysis of bacteria isolated from sole of shoes samples

Echireshia coli LN558643.1

Escherichia coli partial 16S rRNA gene, isolate RS1

Sequence ID: emb|LN558643.1| **Length:** 1484 **Number of Matches:** 1

Range 1: 87 to 1069 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1710 bits(1896)	0.0	972/983(99%)	5/983(0%)	Plus/Plus

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Query  1     AACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGG  60
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Sbjct  87    AACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGG  146

Query  61    CATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAAT  120
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Sbjct  147   CATTCTGATCCACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAAT  206

Query  121   CCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTAT  180
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Sbjct  207   CCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTTTGTAT  266

Query  181   GCGCCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCC  240
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Sbjct  267   GCGCCATTGTAGCACGTGTGTAGCCCTGGTCGTAAGGGCCATGATGACTTGACGTCATCC  326

Query  241   CCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGGACCGCTGGCA  300
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Sbjct  327   CCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCGGACCGCTGGCA  386

Query  301   ACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTG  360
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Sbjct  387   ACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACGAGCTG  446

Query  361   ACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGGCACCAATCCATCTCTGGAAAG  420
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Sbjct  447   ACGACAGCCATGCAGCACCTGTCTCACAGTTCCCGAAGGCACCAATCCATCTCTGGAAAG  506

Query  421   TTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCT  480
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Sbjct  507   TTCTGTGGATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCT  566

Query  481   CCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCC  540
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Sbjct  567   CCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCC  626

Query  541   CAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAG  600
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Sbjct  627   CAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCTCCAAG  686

Query  601   TCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT  660
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Sbjct  687   TCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTT  746

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   CGCACCTGAGCGTCAGTCTTCGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTCCAGAT  806

Query  721   CTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACGAGACTCAAGCTTGC  780
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Sbjct  807   CTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACGAGACTCAAGCTTGC  866

Query  781   CAGTATCAGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCG  840
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Sbjct  867   CAGTATCAGATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTAACAAACCG  926

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             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  927   CCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCCTCCGTATTACCGCG  986

Query  900   GCTGCTGGCACGGAATTAGCCGGGGCTTC-TCTGGGGGTAACGTCAATGAAC-AAGGTAT  957
             ||||||||||||||| |||||||| ||||| |||| |||||||||||||||| |||||||
Sbjct  987   GCTGCTGGCACGGAGTTAGCCGGTGCTTCTTCTGCGGGTAACGTCAATGAACAAAGGTAT  1046

Query  958   TA--CTTACTCCCTTccccccccc  978
             ||   ||||||||||||  ||||
Sbjct  1047  TAACTTTACTCCCTTCCTTCCCC  1069
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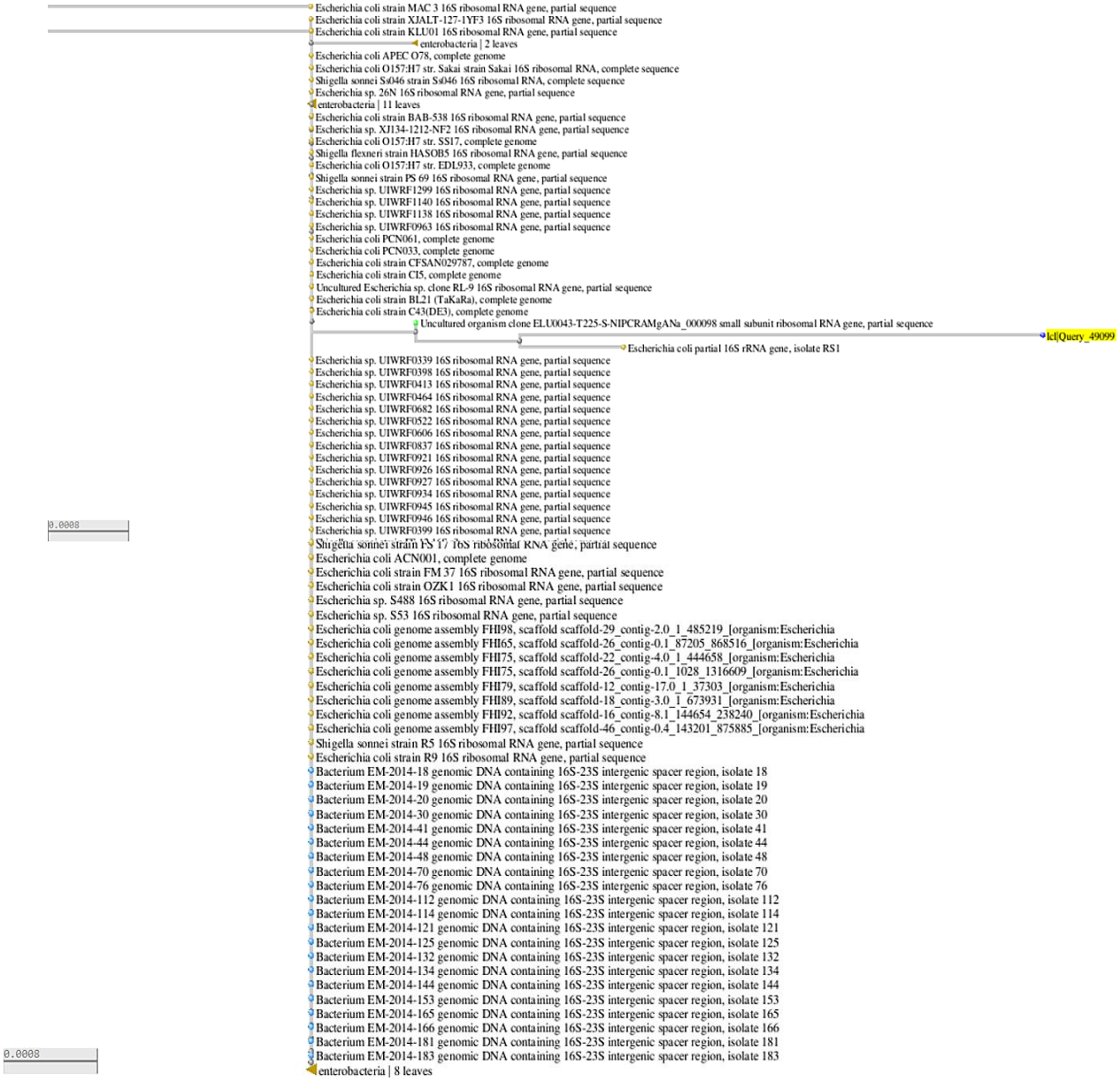
Escherichia coli strain MAC 3 16S ribosomal RNA gene, partial sequence
Escherichia coli strain XJALT-127-1YF3 16S ribosomal RNA gene, partial sequence
Escherichia coli strain KLU01 16S ribosomal RNA gene, partial sequence
enterobacteria | 2 leaves
Escherichia coli APEC O78, complete genome
Escherichia coli O157:H7 str. Sakai strain Sakai 16S ribosomal RNA, complete sequence
Shigella sonnei Ss046 strain Ss046 16S ribosomal RNA, complete sequence
Escherichia sp. 26N 16S ribosomal RNA gene, partial sequence
enterobacteria | 11 leaves
Escherichia coli strain BAB-538 16S ribosomal RNA gene, partial sequence
Escherichia sp. XJ134-1212-NF2 16S ribosomal RNA gene, partial sequence
Escherichia coli O157:H7 str. SS17, complete genome
Shigella flexneri strain HASOB5 16S ribosomal RNA gene, partial sequence
Escherichia coli O157:H7 str. EDL933, complete genome
Shigella sonnei strain PS 69 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF1299 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF1140 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF1138 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0963 16S ribosomal RNA gene, partial sequence
Escherichia coli PCN061, complete genome
Escherichia coli PCN033, complete genome
Escherichia coli strain CFSAN029787, complete genome
Escherichia coli strain CI5, complete genome
Uncultured Escherichia sp. clone RL-9 16S ribosomal RNA gene, partial sequence
Escherichia coli strain BL21 (TaKaRa), complete genome
Escherichia coli strain C43(DE3), complete genome
Uncultured organism clone ELU0043-T225-S-NIPCRAMgANa_000098 small subunit ribosomal RNA gene, partial sequence
kcl|Query_49099
Escherichia coli partial 16S rRNA gene, isolate RS1
Escherichia sp. UIWRF0339 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0398 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0413 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0464 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0682 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0522 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0606 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0837 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0921 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0926 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0927 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0934 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0945 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0946 16S ribosomal RNA gene, partial sequence
Escherichia sp. UIWRF0399 16S ribosomal RNA gene, partial sequence
0.0008
Shigella sonnei strain FS 17 16S ribosomal RNA gene, partial sequence
Escherichia coli ACN001, complete genome
Escherichia coli strain FM 37 16S ribosomal RNA gene, partial sequence
Escherichia coli strain OZK1 16S ribosomal RNA gene, partial sequence
Escherichia sp. S488 16S ribosomal RNA gene, partial sequence
Escherichia sp. S53 16S ribosomal RNA gene, partial sequence
Escherichia coli genome assembly FHI98, scaffold scaffold-29_contig-2.0_1_485219_[organism:Escherichia
Escherichia coli genome assembly FHI65, scaffold scaffold-26_contig-0.1_87205_868516_[organism:Escherichia
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Escherichia coli genome assembly FHI75, scaffold scaffold-26_contig-0.1_1028_1316609_[organism:Escherichia
Escherichia coli genome assembly FHI79, scaffold scaffold-12_contig-17.0_1_37303_[organism:Escherichia
Escherichia coli genome assembly FHI89, scaffold scaffold-18_contig-3.0_1_673931_[organism:Escherichia
Escherichia coli genome assembly FHI92, scaffold scaffold-16_contig-8.1_144654_238240_[organism:Escherichia
Escherichia coli genome assembly FHI97, scaffold scaffold-46_contig-0.4_143201_875885_[organism:Escherichia
Shigella sonnei strain R5 16S ribosomal RNA gene, partial sequence
Escherichia coli strain R9 16S ribosomal RNA gene, partial sequence
Bacterium EM-2014-18 genomic DNA containing 16S-23S intergenic spacer region, isolate 18
Bacterium EM-2014-19 genomic DNA containing 16S-23S intergenic spacer region, isolate 19
Bacterium EM-2014-20 genomic DNA containing 16S-23S intergenic spacer region, isolate 20
Bacterium EM-2014-30 genomic DNA containing 16S-23S intergenic spacer region, isolate 30
Bacterium EM-2014-41 genomic DNA containing 16S-23S intergenic spacer region, isolate 41
Bacterium EM-2014-44 genomic DNA containing 16S-23S intergenic spacer region, isolate 44
Bacterium EM-2014-48 genomic DNA containing 16S-23S intergenic spacer region, isolate 48
Bacterium EM-2014-70 genomic DNA containing 16S-23S intergenic spacer region, isolate 70
Bacterium EM-2014-76 genomic DNA containing 16S-23S intergenic spacer region, isolate 76
Bacterium EM-2014-112 genomic DNA containing 16S-23S intergenic spacer region, isolate 112
Bacterium EM-2014-114 genomic DNA containing 16S-23S intergenic spacer region, isolate 114
Bacterium EM-2014-121 genomic DNA containing 16S-23S intergenic spacer region, isolate 121
Bacterium EM-2014-125 genomic DNA containing 16S-23S intergenic spacer region, isolate 125
Bacterium EM-2014-132 genomic DNA containing 16S-23S intergenic spacer region, isolate 132
Bacterium EM-2014-134 genomic DNA containing 16S-23S intergenic spacer region, isolate 134
Bacterium EM-2014-144 genomic DNA containing 16S-23S intergenic spacer region, isolate 144
Bacterium EM-2014-153 genomic DNA containing 16S-23S intergenic spacer region, isolate 153
Bacterium EM-2014-165 genomic DNA containing 16S-23S intergenic spacer region, isolate 165
Bacterium EM-2014-166 genomic DNA containing 16S-23S intergenic spacer region, isolate 166
Bacterium EM-2014-181 genomic DNA containing 16S-23S intergenic spacer region, isolate 181
Bacterium EM-2014-183 genomic DNA containing 16S-23S intergenic spacer region, isolate 183
0.0008
enterobacteria | 8 leaves

Brevibacillus borstelensis KT239000.1

Brevibacillus borstelensis strain HMR16 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT239000.1| **Length:** 1408 **Number of Matches:** 1

Range 1: 46 to 1030 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1676 bits(1858)	0.0	966/985(98%)	4/985(0%)	Plus/Plus

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Query  1     GAGTAACACGTAGGCAACCTGCCCGTAAGCTCGGGATAACATGGGGAAACTCATGCTAAT  60
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Sbjct  46    GAGTAACACGTAGGCAACCTGCCCGTAAGCTCGGGATAACATGGGGAAACTCATGCTAAT  105

Query  61    ACCGGATAGGGTCTTCTCTCGCATGAGAGGAGACGGAAAGGTGGCGCAAGCTACCACTTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  106   ACCGGATAGGGTCTTCTCTCGCATGAGAGGAGACGGAAAGGTGGCGCAAGCTACCACTTA  165

Query  121   CGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166   CGGATGGGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATG  225

Query  181   CGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  226   CGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTA  285

Query  241   CGGGAGGCAGCAGTAGGGAATTTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCG  300
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Sbjct  286   CGGGAGGCAGCAGTAGGGAATTTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCG  345

Query  301   TGAACGATGAAGGTCTTCGGATTGTAAAGTTCTGTTGTCAGAGACGAACAAGTACCGTTC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346   TGAACGATGAAGGTCTTCGGATTGTAAAGTTCTGTTGTCAGAGACGAACAAGTACCGTTC  405

Query  361   GAACAGGGCGGTACCTTGACGGTACCTGACGAGAAAGCCACGGCTAACTACGTGCCAGCA  420
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Sbjct  406   GAACAGGGCGGTACCTTGACGGTACCTGACGAGAAAGCCACGGCTAACTACGTGCCAGCA  465

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Sbjct  466   GCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCA  525

Query  481   GGCGGCTATGTAAGTCTGGTGTTAAAGCCCGGGGCTCAACCCCGGTTCGCATCGGAAACT  540
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Sbjct  526   GGCGGCTATGTAAGTCTGGTGTTAAAGCCCGGGGCTCAACCCCGGTTCGCATCGGAAACT  585

Query  541   GTGTAGCTTGAGTGCAGAAGAGGAAAGCGGTATTCCACGTGTAGCGGTGAAATGCGTAGA  600
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Sbjct  586   GTGTAGCTTGAGTGCAGAAGAGGAAAGCGGTATTCCACGTGTAGCGGTGAAATGCGTAGA  645

Query  601   GATGTGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGTCTGTAACTGACGCTGAGGCGC  660
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Sbjct  646   GATGTGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGTCTGTAACTGACGCTGAGGCGC  705

Query  661   GAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGT  720
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Sbjct  706   GAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGT  765

Query  721   GCTAGGTGTTGGGGGTTTCAATACCCTCAGTGCCGCAGCTAACGCAATAAGCACTCCGCC  780
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Sbjct  766   GCTAGGTGTTGGGGGTTTCAATACCCTCAGTGCCGCAGCTAACGCAATAAGCACTCCGCC  825

Query  781   TGGGGAGTACGCTCGCAAGAGTGAAACTCAAAGGATTTGACGGGGGCCCGCACAAGCGG-  839
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  826   TGGGGAGTACGCTCGCAAGAGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGT  885

Query  840   GGAGCATGTGGTTTAATTCAAAGCAACGCGAAAAACCTTACCA-GTCTTGACATCCCGCT  898
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Sbjct  886   GGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGCT  945

Query  899   GACCGTCCTaaaaaaaGGGCTTCCCTTC-GGGCAGCGG-GACggggggggCATGGTTGTC  956
             |||||||||| | | |||||||||||||| ||||||||| ||| || || ||||||||||
Sbjct  946   GACCGTCCTAGAGATAGGGCTTCCCTTCGGGGCAGCGGTGACAGGTGGTGCATGGTTGTC  1005

Query  957   GTCCCCTCGGGTCGGGAAATGTGGG  981
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Sbjct  1006  GTCAGCTCGTGTCGTGAGATGTTGG  1030
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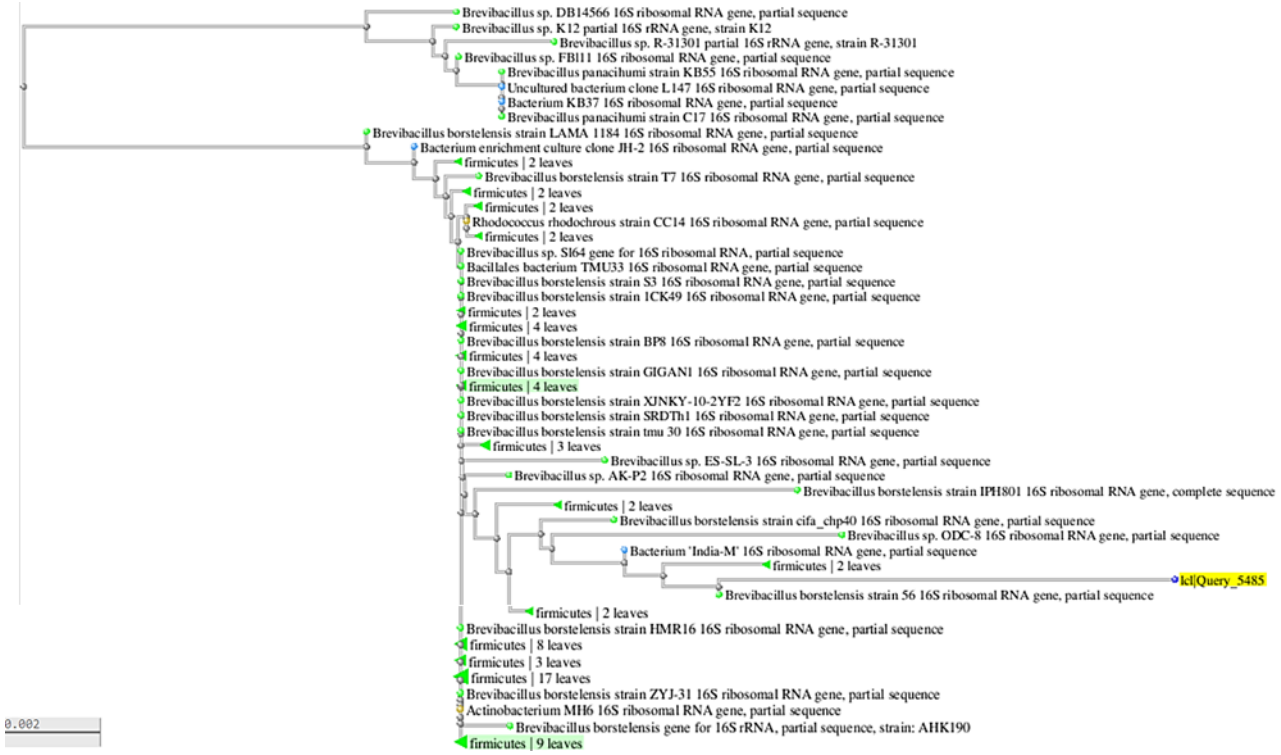
Brevibacillus sp. DB14566 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. K12 partial 16S rRNA gene, strain K12
Brevibacillus sp. R-31301 partial 16S rRNA gene, strain R-31301
Brevibacillus sp. FB111 16S ribosomal RNA gene, partial sequence
Brevibacillus panacihumi strain KB55 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L147 16S ribosomal RNA gene, partial sequence
Bacterium KB37 16S ribosomal RNA gene, partial sequence
Brevibacillus panacihumi strain C17 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain LAMA 1184 16S ribosomal RNA gene, partial sequence
Bacterium enrichment culture clone JH-2 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Brevibacillus borstelensis strain T7 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 2 leaves
Rhodococcus rhodochrous strain CC14 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Brevibacillus sp. SI64 gene for 16S ribosomal RNA, partial sequence
Bacillales bacterium TMU33 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain S3 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain 1CK49 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 4 leaves
Brevibacillus borstelensis strain BP8 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Brevibacillus borstelensis strain GIGAN1 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Brevibacillus borstelensis strain XJNKY-10-2YF2 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain SRDTh1 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain tmu 30 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Brevibacillus sp. ES-SL-3 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. AK-P2 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis strain IPH1801 16S ribosomal RNA gene, complete sequence
firmicutes | 2 leaves
Brevibacillus borstelensis strain cifa_chp40 16S ribosomal RNA gene, partial sequence
Brevibacillus sp. ODC-8 16S ribosomal RNA gene, partial sequence
Bacterium 'India-M' 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
lcl|Query_5485
Brevibacillus borstelensis strain 56 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Brevibacillus borstelensis strain HMR16 16S ribosomal RNA gene, partial sequence
firmicutes | 8 leaves
firmicutes | 3 leaves
firmicutes | 17 leaves
Brevibacillus borstelensis strain ZYJ-31 16S ribosomal RNA gene, partial sequence
Actinobacterium MH6 16S ribosomal RNA gene, partial sequence
Brevibacillus borstelensis gene for 16S rRNA, partial sequence, strain: AHK190
firmicutes | 9 leaves
0.002

Bacillus licheniformis KP772335.1

Bacillus licheniformis strain OALB2 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KP772335.1| **Length:** 1445 **Number of Matches:** 1

Range 1: 45 to 989 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
1645 bits(1824)	0.0	935/945(99%)	4/945(0%)	Plus/Plus

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Sbjct  45   GGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAA  104

Query  61   CCGGGGCTAATACCGGATGCTTGATTGAACCGCATGGTTCAATTATAAAAGGTGGCTTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  105  CCGGGGCTAATACCGGATGCTTGATTGAACCGCATGGTTCAATTATAAAAGGTGGCTTTC  164

Query  121  AGCTACCACTTGCAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165  AGCTACCACTTGCAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACC  224

Query  181  AAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  225  AAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGG  284

Query  241  CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  285  CCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGG  344

Query  301  AGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGGGAAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  345  AGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGGGAAGAA  404

Query  361  CAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  405  CAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAAC  464

Query  421  TACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  465  TACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGT  524

Query  481  AAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525  AAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGG  584

Query  541  GTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  585  GTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGG  644

Query  601  TGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  645  TGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACT  704

Query  661  GACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  705  GACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC  764

Query  721  GTAAACGATGAGTGCTAAGTGTTAAAGGGTTTCCGCCCTTTAGTGCTGCAGCAAACGCAT  780
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  765  GTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCAAACGCAT  824

Query  781  TAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTC-AAGGAATTGACGGGGGC  839
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  825  TAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGC  884

Query  840  CCGCCCAAGCGGGGGAGCATGTGGTTTAATTCGAAGCAACGCGAA-AACCTTACCA-GTC  897
            |||| ||||||| ||||||||||||||||||||||||||||||| |||||||||| |||
Sbjct  885  CCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTC  944

Query  898  TTGACTTCCTCTGAC-ACCCTAAAAATAGGGCTTCCCCTTCGGGG  941
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Sbjct  945  TTGACATCCTCTGACAACCCTAGAGATAGGGCTTCCCCTTCGGGG  989
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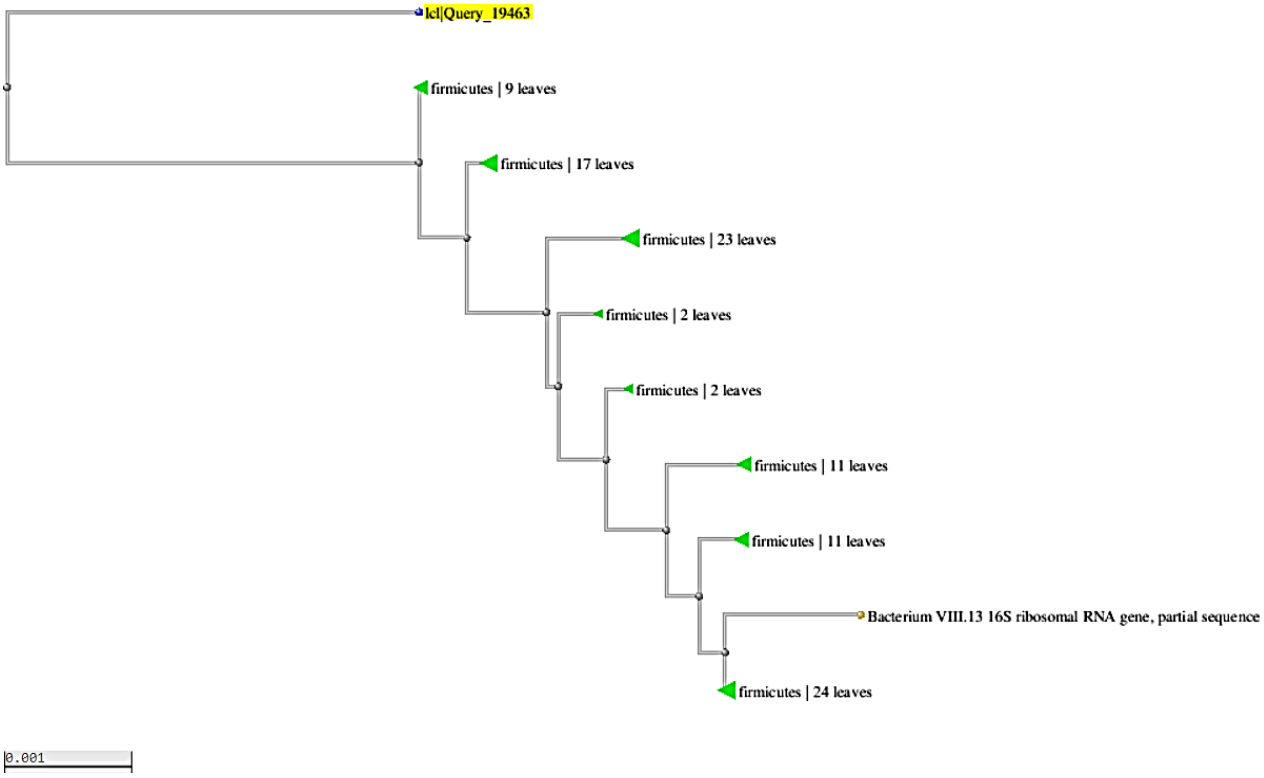
lcl|Query_19463
firmicutes | 9 leaves
firmicutes | 17 leaves
firmicutes | 23 leaves
firmicutes | 2 leaves
firmicutes | 2 leaves
firmicutes | 11 leaves
firmicutes | 11 leaves
Bacterium VIII.13 16S ribosomal RNA gene, partial sequence
firmicutes | 24 leaves
0.001

Enterococcus mundtii KR085796.1

Enterococcus mundtii strain IHBB 9250 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KR085796.1| **Length:** 1518 **Number of Matches:** 1

Range 1: 81 to 1033 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1674 bits(1856)	0.0	944/953(99%)	1/953(0%)	Plus/Plus

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Query  1     CCGGGAAAAGAGGAGTGGCGAACGGGTGAGTAACACGTGGGTAACCTGCCCATCAGAAGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    CCGGGAAAAGAGGAGTGGCGAACGGGTGAGTAACACGTGGGTAACCTGCCCATCAGAAGG  140

Query  61    GGATAACACTTGGAAACAGGTGCTAATACCGTATAACAATCGAAACCGCATGGTTTCGTT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   GGATAACACTTGGAAACAGGTGCTAATACCGTATAACAATCGAAACCGCATGGTTTCGTT  200

Query  121   TTGAAAGGCGCTTTACGGTGCCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   TTGAAAGGCGCTTTACGGTGCCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTG  260

Query  181   AGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACATT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   AGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACATT  320

Query  241   GGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGG  380

Query  301   ACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCT  360
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Sbjct  381   ACGAAAGTCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCT  440

Query  361   GTTGTTAGAGAAGAACAAGGGTGAGAGTAACTGTTCACCCCTTGACGGTATCTAACCAGA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GTTGTTAGAGAAGAACAAGGGTGAGAGTAACTGTTCACCCCTTGACGGTATCTAACCAGA  500

Query  421   AAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   AAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCG  560

Query  481   GATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   GATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGG  620

Query  541   CTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAAT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  621   CTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAAT  680

Query  601   TCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   TCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTC  740

Query  661   TCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCC  800

Query  721   TGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   TGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGC  860

Query  781   TGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  861   TGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG  920

Query  841   GAATTGACGGGGGCCCGCACAAGCGGGGGAGCATGGGGTTTAATTCGAAGCAACGCGAAA  900
             |||||||||||||||||||||||||| ||||||||  ||||||||||||||||||||||||
Sbjct  921   GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAG  980

Query  901   AACCTTACCA-GTCTTGACATCCTTTGACCCCTCTaaaaaaaaaGCTTCCCCT  952
             |||||||||| |||||||||||||||||||| ||||| | | | ||||||||||
Sbjct  981   AACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTCCCCT  1033
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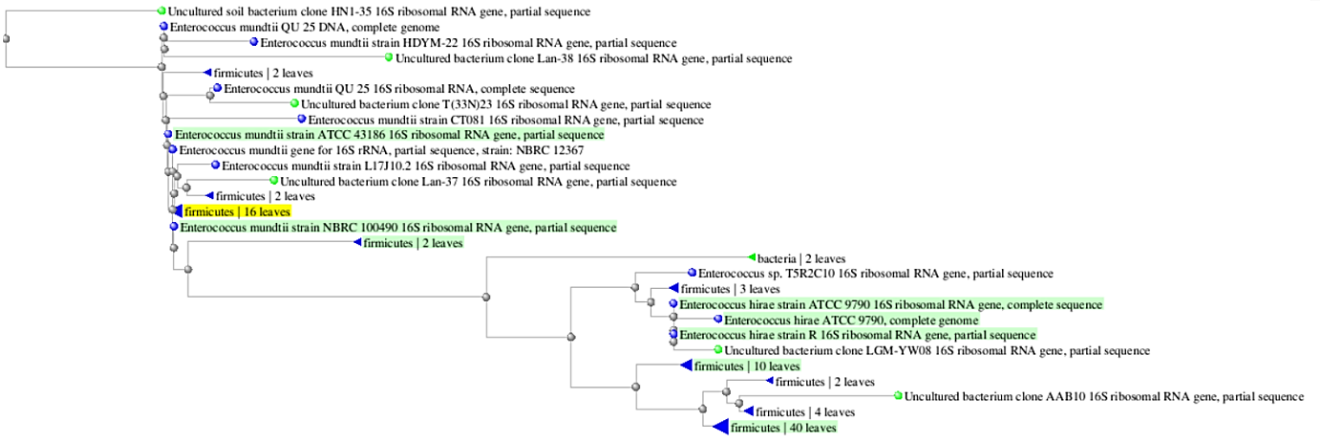
Uncultured soil bacterium clone HN1-35 16S ribosomal RNA gene, partial sequence
Enterococcus mundtii QU 25 DNA, complete genome
Enterococcus mundtii strain HDYM-22 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone Lan-38 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Enterococcus mundtii QU 25 16S ribosomal RNA, complete sequence
Uncultured bacterium clone T(33N)23 16S ribosomal RNA gene, partial sequence
Enterococcus mundtii strain CT081 16S ribosomal RNA gene, partial sequence
Enterococcus mundtii strain ATCC 43186 16S ribosomal RNA gene, partial sequence
Enterococcus mundtii gene for 16S rRNA, partial sequence, strain: NBRC 12367
Enterococcus mundtii strain L17J10.2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone Lan-37 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 16 leaves
Enterococcus mundtii strain NBRC 100490 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
bacteria | 2 leaves
Enterococcus sp. T5R2C10 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Enterococcus hirae strain ATCC 9790 16S ribosomal RNA gene, complete sequence
Enterococcus hirae ATCC 9790, complete genome
Enterococcus hirae strain R 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone LGM-YW08 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
firmicutes | 2 leaves
Uncultured bacterium clone AAB10 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
firmicutes | 40 leaves

Enterococcus hirae KT261200.1

Enterococcus hirae strain RCB988 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT261200.1| **Length:** 1437 **Number of Matches:** 1

Range 1: 59 to 965 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1546 bits(1714)	0.0	892/910(98%)	4/910(0%)	Plus/Plus

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Query  1    AGTAACACGTGGGTAACCTGCCCATCAGAAGGGGATAACACTTGGAAACAGGTGCTAATA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  59   AGTAACACGTGGGTAACCTGCCCATCAGAAGGGGATAACACTTGGAAACAGGTGCTAATA  118

Query  61   CCGTATAACAATCGAAACCGCATGGTTTTGATTTGAAAGGCGCTTTCGGGTGTCGCTGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  119  CCGTATAACAATCGAAACCGCATGGTTTTGATTTGAAAGGCGCTTTCGGGTGTCGCTGAT  178

Query  121  GGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCCACGATGC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  179  GGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGC  238

Query  181  ATAGCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239  ATAGCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTAC  298

Query  241  GGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAGCAACGCCGCGT  300
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Sbjct  299  GGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAGCAACGCCGCGT  358

Query  301  GAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACAAGGATGAGAGT  360
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Sbjct  359  GAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACAAGGATGAGAGT  418

Query  361  AACTGTTCATCCCTTGACGGTATCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419  AACTGTTCATCCCTTGACGGTATCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGC  478

Query  421  CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479  CGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGG  538

Query  481  CGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  539  CGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTG  598

Query  541  GGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAT  600
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Sbjct  599  GGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAT  658

Query  601  ATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCG  660
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Sbjct  659  ATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCG  718

Query  661  AAAGCGTGGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719  AAAGCGTGGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGT  778

Query  721  GCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCTAACGCATTAAACACTCCGCC  780
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Sbjct  779  GCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCTAACGCATTAAGCACTCCGCC  838

Query  781  TGGGGAGTACAACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGGCCGCACAAGCGGT  840
            |||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  839  TGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGT  898

Query  841  GGGAACTTGTGGTTTAATTTCAAACCAACCCaaaaaaaCCTTACCAGG-CTTGAATTCCT  899
             ||| | |||||||||| ||| || |||| |  || ||||||||||| |||||  ||||
Sbjct  899  -GGAGCATGTGGTTTAA-TTCGAAGCAACGC-GAAGAACCTTACCAGGTCTTGACATCCT  955

Query  900  TTGACCCCTC  909
            |||||| |||
Sbjct  956  TTGACCACTC  965
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lcl|Query_8343
firmicutes | 2 leaves
Enterococcus durans strain SJU18 16S ribosomal RNA gene, partial sequence
Enterococcus lactis strain CGLBL160 16S ribosomal RNA gene, partial sequence
Enterococcus lactis partial 16S rRNA gene, strain qz-548
Enterococcus faecalis strain TS4E2 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain KS3S1 16S ribosomal RNA gene, partial sequence
Enterococcus faecium gene for 16S ribosomal RNA, partial sequence, isolate: VMCU54N
Enterococcus faecium strain D 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain AT15 16S ribosomal RNA gene, partial sequence
Enterococcus sp. 55B 16S ribosomal RNA gene, partial sequence
Enterococcus faecium 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain S.156 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-200 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-158 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-156 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-152 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-150 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V9-147 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V6-112 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V6-110 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain E0-190 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V3-101 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain E0-192 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V3-82 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V3-80 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain E3-67 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain E3-66 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V12-65 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V12-25 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain V12-20 16S ribosomal RNA gene, partial sequence
Lactobacillus helveticus strain GM2 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain gp39 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain gp85 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain gp58 16S ribosomal RNA gene, partial sequence
Enterococcus lactis strain SCEN1403 16S ribosomal RNA gene, partial sequence
Enterococcus lactis strain SCEN1402 16S ribosomal RNA gene, partial sequence
Enterococcus lactis strain SCEN1401 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain Z1I 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain YPG 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain YPT 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain YP 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain WVS333 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain BIBT_VC_1 16S ribosomal RNA gene, partial sequence
Enterococcus hirae strain CSCWL2-12 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain PSB 5 16S ribosomal RNA gene, partial sequence
Bacterium QHB36 16S ribosomal RNA gene, partial sequence
Bacterium QHB33 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain SM67 16S ribosomal RNA gene, partial sequence
Uncultured Enterococcus sp. clone 58 16S ribosomal RNA gene, partial sequence
Uncultured Enterococcus sp. clone 13 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain Z4-21 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain CA13 16S ribosomal RNA gene, complete sequence
Enterococcus faecium strain CA03-1 16S ribosomal RNA gene, complete sequence
Bacterium P2A5 16S ribosomal RNA gene, partial sequence
Bacterium P2E9 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain KLDS 6.0933 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain KDLLJ2-1 16S ribosomal RNA gene, partial sequence
Enterococcus hirae strain RCB988 16S ribosomal RNA gene, partia
Bacterium MRG-FC-3 16S ribosomal RNA gene, partial sequence
firmicutes | 9 leaves
Bacterium SJD 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain TPBLGL 30 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain SAMBN-4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2_57_1421 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain SMN I-2 16S ribosomal RNA gene, partial sequence
Enterococcus hirae strain C07_1387_03 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF07 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF01 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF03 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF04 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF06 16S ribosomal RNA gene, partial sequence
Enterococcus sp. QAUEF05 16S ribosomal RNA gene, partial sequence
Enterococcus sp. MRSA78B1_13_1A 16S ribosomal RNA gene, partial sequence
Enterococcus sp. MRSA87B1_13_1A 16S ribosomal RNA gene, partial sequence
Enterococcus sp. MRSA93B1_13_2E 16S ribosomal RNA gene, partial sequence
Enterococcus sp. MRSA145B15_13_2E 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain IMAU11163 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain IMAU11167 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain IMAU11650 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain IMAU11652 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain IMAU11658 16S ribosomal RNA gene, partial sequence
Enterococcus faecalis strain NK1 16S ribosomal RNA gene, partial sequence
Enterococcus faecium strain NK8 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain IMAU11458 (DM17-3) 16S ribosomal RNA gene, partial sequence
Enterococcus durans strain IMAU11321 (YM36-10) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 4L1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 3L6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2L3 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Enterococcus faecium strain 64/3, complete genome
0.0008
0.0008

Bacillus licheniformis DQ071560.1

Bacillus licheniformis strain MKU 1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|DQ071560.1| **Length:** 1430 **Number of Matches:** 1

Range 1: 431 to 1393 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1703 bits(1888)	0.0	958/963(99%)	3/963(0%)	Plus/Minus

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Query  1     TTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCG  60
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Sbjct  1393  TTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCG  1334

Query  61    GCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGA  120
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Sbjct  1333  GCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGA  1274

Query  121   TCCGAACTGAGAACAGATTTGTGGGATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1273  TCCGAACTGAGAACAGATTTGTGGGATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTT  1214

Query  181   CTGCCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1213  CTGCCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC  1154

Query  241   CCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1153  CCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCA  1094

Query  301   ACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1093  ACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTG  1034

Query  361   ACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1033  ACGACAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTT  974

Query  421   GTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  973   GTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCT  914

Query  481   CCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  913   CCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCC  854

Query  541   CAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTAAAGGGCGGAAACCCTCTAACACTTA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  853   CAGGCGGAGTGCTTAATGCGTTTGCTGCAGCACTAAAGGGCGGAAACCCTCTAACACTTA  794

Query  601   GCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  793   GCACTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTT  734

Query  661   TCGCGCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACA  720
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Sbjct  733   TCGCGCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACA  674

Query  721   TCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  673   TCTCTACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCC  614

Query  781   CCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  613   CCAGTTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACC  554

Query  841   GCCTGCGCGCGCTTTACGCCCAATAATTCCGGA-AACGCTTGCCCCCTACGTATTACCGC  899
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Sbjct  553   GCCTGCGCGCGCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGC  494

Query  900   GGCTGCTGGCACGTAGTTAGCCGGGGCTTTCTGGTTAGGTACCGTC-AGGTACC-CCCTA  957
             |||||||||||||||||||| |||||||||||||||||||| ||||||| |||||
Sbjct  493   GGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTACCGCCCTA  434

Query  958   TTC  960
             |||
Sbjct  433   TTC  431
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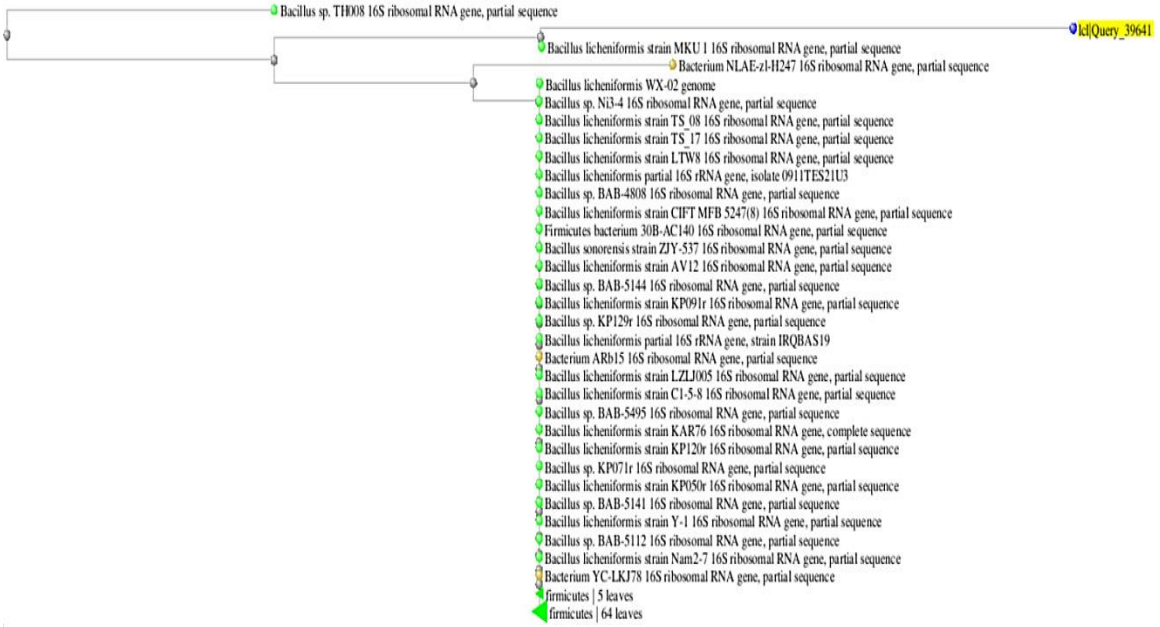
Bacillus sp. TH008 16S ribosomal RNA gene, partial sequence
lcl|Query_39641
Bacillus licheniformis strain MKU 1 16S ribosomal RNA gene, partial sequence
Bacterium NLAE-zl-H247 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis WX-02 genome
Bacillus sp. Ni3-4 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain TS_08 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain TS_17 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain LTW8 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis partial 16S rRNA gene, isolate 0911TES21U3
Bacillus sp. BAB-4808 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CIFT MFB 5247(8) 16S ribosomal RNA gene, partial sequence
Firmicutes bacterium 30B-AC140 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain ZJY-537 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain AV12 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5144 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP091r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP129r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS19
Bacterium ARb15 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain LZLJ005 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain C1-5-8 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5495 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KAR76 16S ribosomal RNA gene, complete sequence
Bacillus licheniformis strain KP120r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP071r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP050r 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5141 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Y-1 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5112 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Nam2-7 16S ribosomal RNA gene, partial sequence
Bacterium YC-LKJ78 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
firmicutes | 64 leaves

Lysinibacillus fusiformis KP872952.1

Lysinibacillus fusiformis strain XKS50.1 16S ribosomal RNA gene, partial sequence

Sequence ID: KP872952.1 Length: 1450 Number of Matches: 1

Range 1: 1 to 1450 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
2678 bits(1450)	0.0	1450/1450(100%)	0/1450(0%)	Plus/Plus

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Sbjct  1     CCCGGGGGGGTCCTATACATGCAAGTCGAGCGAACAGAAAAGGAGCTTGCTCCTTTGACGT  60

Query  61    TAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGG  120
Sbjct  61    TAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTACCCTATAGTTTGGGATAACTCCGG  120

Query  121   GAAACCGGGGCTAATACCGAATAATCTCTTTTGCTTCATGGTGAAAGACTGAAAGACGGT  180
Sbjct  121   GAAACCGGGGCTAATACCGAATAATCTCTTTTGCTTCATGGTGAAAGACTGAAAGACGGT  180

Query  181   TTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTC  240
Sbjct  181   TTCGGCTGTCGCTATAGGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTC  240

Query  241   ACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACA  300
Sbjct  241   ACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACA  300

Query  301   CGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCTGA  360
Sbjct  301   CGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGGCGAAAGCCTGA  360

Query  361   TGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTAAGGGAA  420
Sbjct  361   TGGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTAAGGGAA  420

Query  421   GAACAAGTACAGTAGTAACTGGCTGTACCTTGACGGTACCTTATTAGAAAGCCACGGCTA  480
Sbjct  421   GAACAAGTACAGTAGTAACTGGCTGTACCTTGACGGTACCTTATTAGAAAGCCACGGCTA  480

Query  481   ACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGC  540
Sbjct  481   ACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGC  540

Query  541   GTAAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGA  600
Sbjct  541   GTAAAGCGCGCGCAGGCGGTCCTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGA  600

Query  601   GGGTCATTGGAAACTGGGGGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAAGTGTAGC  660
Sbjct  601   GGGTCATTGGAAACTGGGGGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCAAGTGTAGC  660

Query  661   GGTGAAATGCGTAGAGATTTGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAA  720
Sbjct  661   GGTGAAATGCGTAGAGATTTGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAA  720

Query  721   CTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG  780
Sbjct  721   CTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG  780

Query  781   CCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGC  840
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Query  841   ATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGG  900
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Query  901   GCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGG  960
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Query  961   TCTTGACATCCCGTTGACCACTGTAGAGATATAGTTTCCCCTTCGGGGGCAACGGTGACA  1020
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Query  1021  GGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG  1080
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Query  1141  CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACA  1200
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Query  1201  CACGTGCTACAATGGACGATACAAACGGTTGCCAACTCGCGAGAGGGAGCTAATCCGATA  1260
Sbjct  1201  CACGTGCTACAATGGACGATACAAACGGTTGCCAACTCGCGAGAGGGAGCTAATCCGATA  1260

Query  1261  AAGTCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCCGGAATCGCTAG  1320
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Query  1321  TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC  1380
Sbjct  1321  TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC  1380

Query  1381  ACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTGGAGCCAGCCGCCGA  1440
Sbjct  1381  ACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTGGAGCCAGCCGCCGA  1440

Query  1441  AGGTGATGAT  1450
Sbjct  1441  AGGTGATGAT  1450
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kl|Query_107117
Bacterium BCL13 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium SE17 16S ribosomal RNA gene, partial sequence
Bacillaceae bacterium SE41 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain GT18 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain BL1 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain BL2 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain BL7 16S ribosomal RNA gene, partial sequence
Bacillus sp. PZ_7 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. enrichment culture clone MJJ-11 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain R3 16S ribosomal RNA gene, partial sequence
Bacillus sp. F8 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain TL 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain Ulm26 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain N169 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain N139 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain LEs06 16S ribosomal RNA gene, partial sequence
Bacillales bacterium Cul_0304 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. JN09 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. SS1.22 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain 44A 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain L13 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain L106 16S ribosomal RNA gene, partial sequence
Geobacillus stearothermophilus strain KS141 16S ribosomal RNA gene, partial sequence
Lysinibacillus boronitolerans clone CrB-L6 16S ribosomal RNA gene, partial sequence
Firmicutes bacterium K17 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. Y20 16S ribosomal RNA gene, complete sequence
Lysinibacillus macroides strain fwzy1 16S ribosomal RNA gene, partial sequence
Lysinibacillus macroides strain fwzy182 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis partial 16S rRNA gene, strain S5
Lysinibacillus macroides partial 16S rRNA gene, isolate AVS1
Proteus mirabilis strain BCr 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. W1.10-228 16S ribosomal RNA gene, complete sequence
Lysinibacillus sp. S-2 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone XT58 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain 164B (BP1) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S ribosomal RNA, partial sequence, clone: 20JB1
Lysinibacillus fusiformis strain S-1 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. XJJC-134-1RF1 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. BAB-2942 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. BAB-637 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain PMM3 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain B1-CDA 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain BD3 16S ribosomal RNA gene, partial sequence
Bacterium BCL19 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb43 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb56 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb60 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. LS-065 16S ribosomal RNA gene, partial sequence
Lysinibacillus macroides isolate Y59 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain 3 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain 4 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain C 16S ribosomal RNA gene, partial sequence
Lysinibacillus macroides strain M0607 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain D 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. 6BK6Y10 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain RNB6 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZGRY2 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. CZGRY3 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZGRY5 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZGRY11 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZGRY13 16S ribosomal RNA gene, partial sequence
Enterobacter sp. CZGRY7 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZGRY8 16S ribosomal RNA gene, partial sequence
Lysinibacillus macroides strain WS26 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain 14AGG21 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain 37POZ32 16S ribosomal RNA gene, partial sequence
Bacillus sp. TG5 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KWW 55
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KWW 56
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KWW 64
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KWW 151
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KSW 19
Lysinibacillus xylanilyticus partial 16S rRNA gene, isolate KSW 23
Lysinibacillus sphaericus strain Xyn-1 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain DZ51 16S ribosomal RNA gene, partial sequence
Bacterium BCL11 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain D27 16S ribosomal RNA gene, partial sequence
Lysinibacillus macroides strain Y-4B 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. BAB-4376 16S ribosomal RNA gene, partial sequence
Lysinibacillus sphaericus strain YH4 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. 3HHX 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain BCH540 16S ribosomal RNA gene, partial sequence
Lysinibacillus xylanilyticus strain A8 16S ribosomal RNA gene, partial sequence
Lysinibacillus sp. DB14380 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S rRNA, partial sequence, clone: CLZX151
Lysinibacillus sp. Vr42 partial 16S rRNA gene, strain Vr42
Lysinibacillus fusiformis strain KAR73 16S ribosomal RNA gene, complete sequence
Lysinibacillus sp. FJAT-22044 16S ribosomal RNA gene, partial sequence
Lysinibacillus fusiformis strain SBB30 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone LX1-B74 16S ribosomal RNA gene, partial sequence
firmicutes | 8 leaves
0.0001

Aneurinibacillus migulanus (Bacillus brevis) NR_113764.1

Aneurinibacillus migulanus strain NBRC 15520 16S ribosomal RNA gene, partial sequence

Sequence ID: ref|NR_113764.1| **Length:** 1464 **Number of Matches:** 1

See 1 more title(s)

Range 1: 28 to 1441 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
2531 bits(2806)	0.0	1411/1414(99%)	2/1414(0%)	Plus/Plus

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Query  18    ATGCA-GTCGAGCGGACCAATGAAGAGCTTGCTCTTCGGCGGTTAGCGGCGGACGGGTGA  76
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Sbjct  28    ATGCAAGTCGAGCGGACCAATGAAGAGCTTGCTCTTCGGCGGTTAGCGGCGGACGGGTGA  87

Query  77    GTAACACGTAGGCAACCTGCCTGTACGACTGGGATAACTCCGGGAAACCGGAGCTAATAC  136
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  88    GTAACACGTAGGCAACCTGCCTGTACGACTGGGATAACTCCGGGAAACCGGAGCTAATAC  147

Query  137   CGGATACTTCTTTCAGACCGCATGGTCTGAAAGGGAAAGACCTTTGGTCACGTACAGATG  196
             |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Sbjct  148   CGGATACTTCTTTCAGACCGCATGGTCTGAAAGGGAAAGACNTTTGGTCACGTACAGATG  207

Query  197   GGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCGTAGC  256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  208   GGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCCTACCAAGGCGACGATGCGTAGC  267

Query  257   CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  316
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Sbjct  268   CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  327

Query  317   GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAACG  376
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Sbjct  328   GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAACG  387

Query  377   ATGAAGGTTTTCGGATCGTAAAGTTCTGTTGTTAGGGAAGAACCGCCGGGATGACCTCCC  436
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Sbjct  388   ATGAAGGTTTTCGGATCGTAAAGTTCTGTTGTTAGGGAAGAACCGCCGGGATGACCTCCC  447

Query  437   GGTCTGACGGTACCTAACGAGAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATA  496
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Sbjct  448   GGTCTGACGGTACCTAACGAGAAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATA  507

Query  497   CGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTA  556
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Sbjct  508   CGTAGGGGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGCTTCTTA  567

Query  557   AGTCAGGTGTGAAAGCCCACGGCTCAACCGTGGAGGGCCACTTGAAACTGGGAAGCTTGA  616
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Sbjct  628   GTGCAGGAGAGGAGAGCGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGA  687

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Query  737   GAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTGAGTGCTAGGTGTTG  796
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Sbjct  748   GAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTGAGTGCTAGGTGTTG  807

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Sbjct  808   GGGACTCCAATCCTCAGTGCCGCAGCTAACGCAATAAGCACTCCGCCTGGGGAGTACGGC  867

Query  857   CGCAAGGCTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTT  916
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Sbjct  868   CGCAAGGCTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTT  927

Query  917   TAATTCGAAGCAACGCGAAGAACCTTACCAGGGCTTGACATCCCGCTGACCCTCCTAGAG  976
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Sbjct  928   TAATTCGAAGCAACGCGAAGAACCTTACCAGGGCTTGACATCCCGCTGACCCTCCTAGAG  987

Query  977   ATAGGAGCTCTCTTCGGAGCAGCGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTC  1036
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Query  1037  GTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTTAGTTGCCAGCATTT  1096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1048  GTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTTAGTTGCCAGCATTT  1107

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Sbjct  1108  AGTTGGGCACTCTAGGGAGACTGCCGTCGACAAGACGGAGGAAGGTGGGGATGACGTCAA  1167

Query  1157  ATCATCATGCCCCTTATGTCCTGGGCTACACACGTGCTACAATGGATGGAACAACGGGCA  1216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1168  ATCATCATGCCCCTTATGTCCTGGGCTACACACGTGCTACAATGGATGGAACAACGGGCA  1227

Query  1217  GCCAACTCGCGAGAGTGCGCGAATCCCTTAAAACCATTCTCAGTTCGGATTGCAGGCTGC  1276
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Sbjct  1228  GCCAACTCGCGAGAGTGCGCGAATCCCTTAAAACCATTCTCAGTTCGGATTGCAGGCTGC  1287

Query  1277  AACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATA  1336
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Query  1337  CGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGCAACACCCGAAGTC  1396
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Sbjct  1348  CGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGCAACACCCGAAGTC  1407

Query  1397  GGTGAGGTAACCGCAA-GAGCCAGCCGCCGAAGG  1429
             ||||||||||||||| ||||||||||||||||
Sbjct  1408  GGTGAGGTAACCGCAAGGAGCCAGCCGCCGAAGG  1441
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Aneurinibacillus sp. U33 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Aneurinibacillus danicus strain NBRC 102444 16S ribosomal RNA gene, partial sequence
Uncultured Bacilli bacterium clone SHBZ1214 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Uncultured bacterium clone 286_TC3_14 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus sp. dcs7 16S ribosomal RNA gene, partial sequence
firmicutes | 27 leaves
Aneurinibacillus migulanus strain SPSU B4 16S ribosomal RNA gene, partial sequence
Aneurinibacillus aneurinilyticus strain y170 16S ribosomal RNA gene, partial sequence
Aneurinibacillus aneurinilyticus strain G7_2_4BCO2 16S ribosomal RNA gene, partial sequence
firmicutes | 8 leaves
firmicutes | 10 leaves
Aneurinibacillus aneurinilyticus gene for 16S rRNA, partial sequence, strain: NBRC 3115
Uncultured prokaryote clone TP60-07 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves

Bacillus subtilis **EF488088.1**

Bacillus subtilis strain QD9 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|EF488088.1| **Length:** 1412 **Number of Matches:** 1

Range 1: 366 to 1319 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1700 bits(1884)	0.0	950/954(99%)	1/954(0%)	Plus/Minus

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Query  1     AAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCAT  60
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Sbjct  1319  AAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCAT  1260

Query  61    GCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCG  120
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Sbjct  1259  GCTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCG  1200

Query  121   AACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTTTGTTCTGT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1199  AACTGAGAACAGATTTGTGGGATTGGCTTAACCTCGCGGTTTCGCTGCCCTTTGTTCTGT  1140

Query  181   CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCA  240
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Sbjct  1139  CCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCA  1080

Query  241   CCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTA  300
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Sbjct  1079  CCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTA  1020

Query  301   AGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGA  360
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Sbjct  1019  AGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGA  960

Query  361   CAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATCTCTAGGATTGTCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  959   CAACCATGCACCACCTGTCACTCTGCCCCCGAAGGGGACGTCCTATCTCTAGGATTGTCA  900

Query  421   GAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCAC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  481   CGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  839   CGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGG  780

Query  541   CGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCAC  600
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Sbjct  779   CGGAGTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCAC  720

Query  601   TCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGC  660
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Sbjct  719   TCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGC  660

Query  661   TCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   TCCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTC  600

Query  721   TACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCCCCAG  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  599   TACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCCCCAG  540

Query  781   TTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACCGCCT  840
             |||||||||||||||||||||||||||||||||||||||||||||  ||||||  |||||||||
Sbjct  539   TTTCCAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCT  480

Query  841   GCGAGCCCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCT  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   GCGAGCCCTTTACGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCT  420

Query  901   GCTGGCACGTAGTTAGCCGGGCTTTCTGGTTAGGTACCGTC-AGGTACCGCCCT  953
             ||||||||||||||||||  ||||||||||||||||||||  ||||||||||||
Sbjct  419   GCTGGCACGTAGTTAGCCGTGCTTTCTGGTTAGGTACCGTCAAGGTACCGCCCT  366
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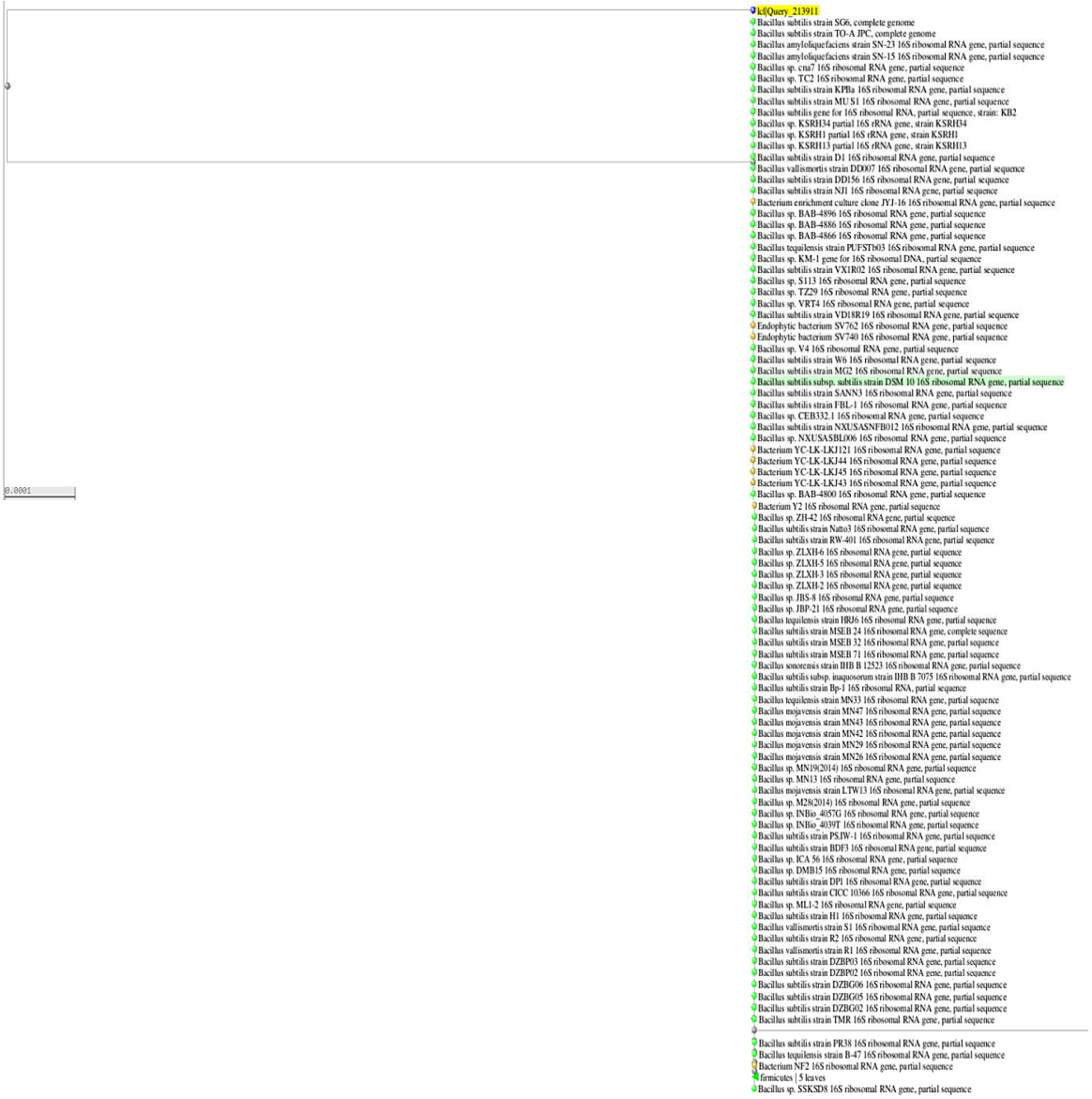
0.0001
kl[Query_213911
Bacillus subtilis strain SG6, complete genome
Bacillus subtilis strain TO-A JPC, complete genome
Bacillus amyloliquefaciens strain SN-23 16S ribosomal RNA gene, partial sequence
Bacillus amyloliquefaciens strain SN-15 16S ribosomal RNA gene, partial sequence
Bacillus sp. cna7 16S ribosomal RNA gene, partial sequence
Bacillus sp. TC2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain KPBa 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MU S1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis gene for 16S ribosomal RNA, partial sequence, strain: KB2
Bacillus sp. KSRH34 partial 16S rRNA gene, strain KSRH34
Bacillus sp. KSRH1 partial 16S rRNA gene, strain KSRH1
Bacillus sp. KSRH13 partial 16S rRNA gene, strain KSRH13
Bacillus subtilis strain D1 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain DD007 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DD156 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain NJ1 16S ribosomal RNA gene, partial sequence
Bacterium enrichment culture clone JYJ-16 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4896 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4886 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4866 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis strain PUFSTb03 16S ribosomal RNA gene, partial sequence
Bacillus sp. KM-1 gene for 16S ribosomal DNA, partial sequence
Bacillus subtilis strain YXIR02 16S ribosomal RNA gene, partial sequence
Bacillus sp. S113 16S ribosomal RNA gene, partial sequence
Bacillus sp. TZ29 16S ribosomal RNA gene, partial sequence
Bacillus sp. VRT4 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain VD18R19 16S ribosomal RNA gene, partial sequence
Endophytic bacterium SV762 16S ribosomal RNA gene, partial sequence
Endophytic bacterium SV740 16S ribosomal RNA gene, partial sequence
Bacillus sp. V4 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain W6 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MG2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. subtilis strain DSM 10 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain SANN3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain FBL-1 16S ribosomal RNA gene, partial sequence
Bacillus sp. CEB332.1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain NXUSASNFB012 16S ribosomal RNA gene, partial sequence
Bacillus sp. NXUSASBL006 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ121 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ44 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ45 16S ribosomal RNA gene, partial sequence
Bacterium YC-LK-LKJ43 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-4800 16S ribosomal RNA gene, partial sequence
Bacterium Y2 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZH-42 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Natto3 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain RW-401 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-6 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-3 16S ribosomal RNA gene, partial sequence
Bacillus sp. ZLXH-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. JBS 8 16S ribosomal RNA gene, partial sequence
Bacillus sp. JBP-21 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis strain HRJ6 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MSEB 24 16S ribosomal RNA gene, complete sequence
Bacillus subtilis strain MSEB 32 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain MSEB 71 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain IHB B 12523 16S ribosomal RNA gene, partial sequence
Bacillus subtilis subsp. inaquosorum strain IHB B 7075 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain Bp-1 16S ribosomal RNA, partial sequence
Bacillus tequilensis strain MN33 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain MN47 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain MN43 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain MN42 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain MN29 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain MN26 16S ribosomal RNA gene, partial sequence
Bacillus sp. MN19(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. MN13 16S ribosomal RNA gene, partial sequence
Bacillus mojavensis strain LTW13 16S ribosomal RNA gene, partial sequence
Bacillus sp. M28(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4057G 16S ribosomal RNA gene, partial sequence
Bacillus sp. INBio_4039T 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PSJW-1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain BDF3 16S ribosomal RNA gene, partial sequence
Bacillus sp. ICA 56 16S ribosomal RNA gene, partial sequence
Bacillus sp. DMB15 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DP1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain CICC 10366 16S ribosomal RNA gene, partial sequence
Bacillus sp. ML1-2 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain H1 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain S1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain R2 16S ribosomal RNA gene, partial sequence
Bacillus vallismortis strain R1 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DZBP03 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DZBP02 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DZBG06 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DZBG05 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain DZBG02 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain TMR 16S ribosomal RNA gene, partial sequence
Bacillus subtilis strain PR38 16S ribosomal RNA gene, partial sequence
Bacillus tequilensis strain B-47 16S ribosomal RNA gene, partial sequence
Bacterium NF2 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus sp. SSKSD8 16S ribosomal RNA gene, partial sequence

8- The phylogenetic analysis of bacteria isolated from books and shelves in libraries and archive storerooms samples.

Pseudomonas jessenii LN774645.1

Pseudomonas jessenii partial 16S rRNA gene, isolate 1111MAR14N4

Sequence ID: emb|LN774645.1| **Length:** 1191 **Number of Matches:** 1

Range 1: 1 to 1028 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1775 bits(1968)	0.0	1013/1028(99%)	3/1028(0%)	Plus/Plus

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Query  16    AATGCCTAGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACCGC  75
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AATGCCTAGGAATCTGCCTATTAGTGGGGGACAACGTTTCGAAAGGAACGCTAATACCGC  60

Query  76    ATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTAATAGATGAGCCTAGG  135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTAATAGATGAGCCTAGG  120

Query  136   TCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCCGTAACTGGTCTGA  195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGACGATCCGTAACTGGTCTGA  180

Query  196   GAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGT  255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGT  240

Query  256   GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGT  315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGT  300

Query  316   CTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTCGTTGCCTAATACGTGACGGTT  375
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  301   CTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTCGTTGCCTAATACGTGACGGCT  360

Query  376   TTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAG  435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAG  420

Query  436   AGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTGTTAAGT  495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTGTTAAGT  480

Query  496   TGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCAAGCTAGAGTA  555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCAAGCTAGAGTA  540

Query  556   CGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACA  615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACA  600

Query  616   TCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAG  675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAG  660

Query  676   C-AACAGGATTAGATACCCTGGTAGTCCACGCCGT-AACGATGTCAACTAGCCGTTGGGA  733
             | ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  661   CAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTTGGGA  720

Query  734   TCCTTGAGATCTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCG  793
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TCCTTGAGATCTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCCTGGGGAGTACGGCCG  780

Query  794   CAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTA  853
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTA  840

Query  854   ATTCGAAGCAACGCGAAAAACCTTACCAGGCCTTGACATCCAGTGAACTTTCCAGAAATG  913
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Sbjct  841   ATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCCAGTGAACTTTCCAGAGATG  900

Query  914   GATTGGTGCCTTCGGGAACACTGAAACAGGGGCTGCATGGCTGTCGTCAGCTCGGGTCGG  973
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Sbjct  901   GATTGGTGCCTTCGGGAACACTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGT  960

Query  974   GAAATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGTCCTTAATTA-CAGCCCGTTA  1032
             || |||||||||||||||||||||||||||||||||||||||||||||| ||| |||| ||| |
Sbjct  961   GAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTAA  1020

Query  1033  AGGGGGGC  1040
             ||| ||||
Sbjct  1021  AGGTGGGC  1028
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Pseudomonas sp. B205-M3 16S ribosomal RNA gene, partial sequence
Gamma proteobacterium RBE2CD-136 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. CL1805 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone HT14 16S ribosomal RNA gene, partial sequence
Pseudomonas putida 16S ribosomal RNA gene, strain: EST1033, partial sequence
Pseudomonas putida strain I5-7 16S ribosomal RNA gene, partial sequence
Bacterium C0038 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. CC91 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Pseudomonas sp. HME6891 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2016d12c1 16S ribosomal RNA gene, partial sequence
Bacterium OC25(2011) 16S ribosomal RNA gene, partial sequence
Uncultured Pseudomonas sp. clone EiT307_C07 16S ribosomal RNA gene, partial seq
Uncultured bacterium clone ncd2070c06c1 16S ribo
g-proteobacteria | 2 leaves
g-proteobacteria | 14 leaves
Uncultured bacterium c
Pseudomonas gingeri strain RBE1CD-71 16S ribosomal R
Pseudomonas putida 16S ribosomal RNA gene, strain: ATCC 11172, partial sequence
g-proteobacteria | 3 leaves
Pseudomonas putida strain ATCC 12633 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 3 leaves
Pseudomonas sp. WSCIII 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw232g03c1 16S ribosomal RNA gene, partial sequence
Pseudomonas putida NBRC 14164 DNA, complete genome
Uncultured bacterium clone ncd405e06c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Pseudomonas putida gene for 16S rRNA, partial sequence, strain: KF715
Pseudomonas putida strain ATCC 17485 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain P1 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain P19 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone MP104-0916-b40 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain ZX-PKU-004 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain PA1 16S ribosomal RNA gene, partial sequence
Pseudomonas putida 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw52a01c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. SJ-4(2011) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone N-167 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. C-S-PDA3 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 2007 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain KUDC1807 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain TCA23 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain M70 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L3-B40 small subunit ribosomal RNA gene, partial sequence
Pseudomonas putida strain C132 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain IR35 16S ribosomal RNA gene, partial sequence
Bacterium MPL30 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain C116 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L3-B18 small subunit ribosomal RNA gene, partial sequence
Pseudomonas putida strain M32 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain n8 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 4049 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. DPs-23 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. C-S-NA6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone N-113 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd503e12c1 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 11 leaves
Pseudomonas sp. GA07 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain IHB B 13625 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone L3-B02 small subunit ribosomal RNA gene, partial sequence
Pseudomonas putida strain M30 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain n7 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 4030 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain SXMAs-6 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. C-S-PDA6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone N-07 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 3 leaves
Pseudomonas alkylphenolia strain G-R-1-1 16S ribosomal RNA gene, partial sequence
0.002
0.002

Bacillus cereus **KP192930.1**

Bacillus cereus strain SHZ3.1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KP192930.1| **Length:** 1419 **Number of Matches:** 1

Range 1: 334 to 1385 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1824 bits(2022)	0.0	1039/1052(99%)	4/1052(0%)	Plus/Minus

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Query  1     CGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTC  60
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Sbjct  1385  CGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTC  1326

Query  61    ACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1325  ACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGC  1266

Query  121   CTACAATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1265  CTACAATCCGAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTC  1206

Query  181   TTTGTACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGAC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1205  TTTGTACCGTCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGAC  1146

Query  241   GTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1145  GTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATG  1086

Query  301   ATGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACAC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1085  ATGGCAACTAAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACAC  1026

Query  361   GAGCTGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCT  420
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Sbjct  1025  GAGCTGACGACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCT  966

Query  421   AGGGTTTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCA  480
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Sbjct  965   AGGGTTTTCAGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCA  906

Query  481   CATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGT  540
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Sbjct  905   CATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGT  846

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Sbjct  605   AGTCTCCCAGTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAA  546

Query  841   AAAACCACCTGCGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTAT  900
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Sbjct  545   GAAACCACCTGCGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTAT  486

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Sbjct  425   AGCTTATTCAACTAGCACTTGTTCTTCCCTAACAACAAAATTTTACGACCCGAAAGCCTT  366

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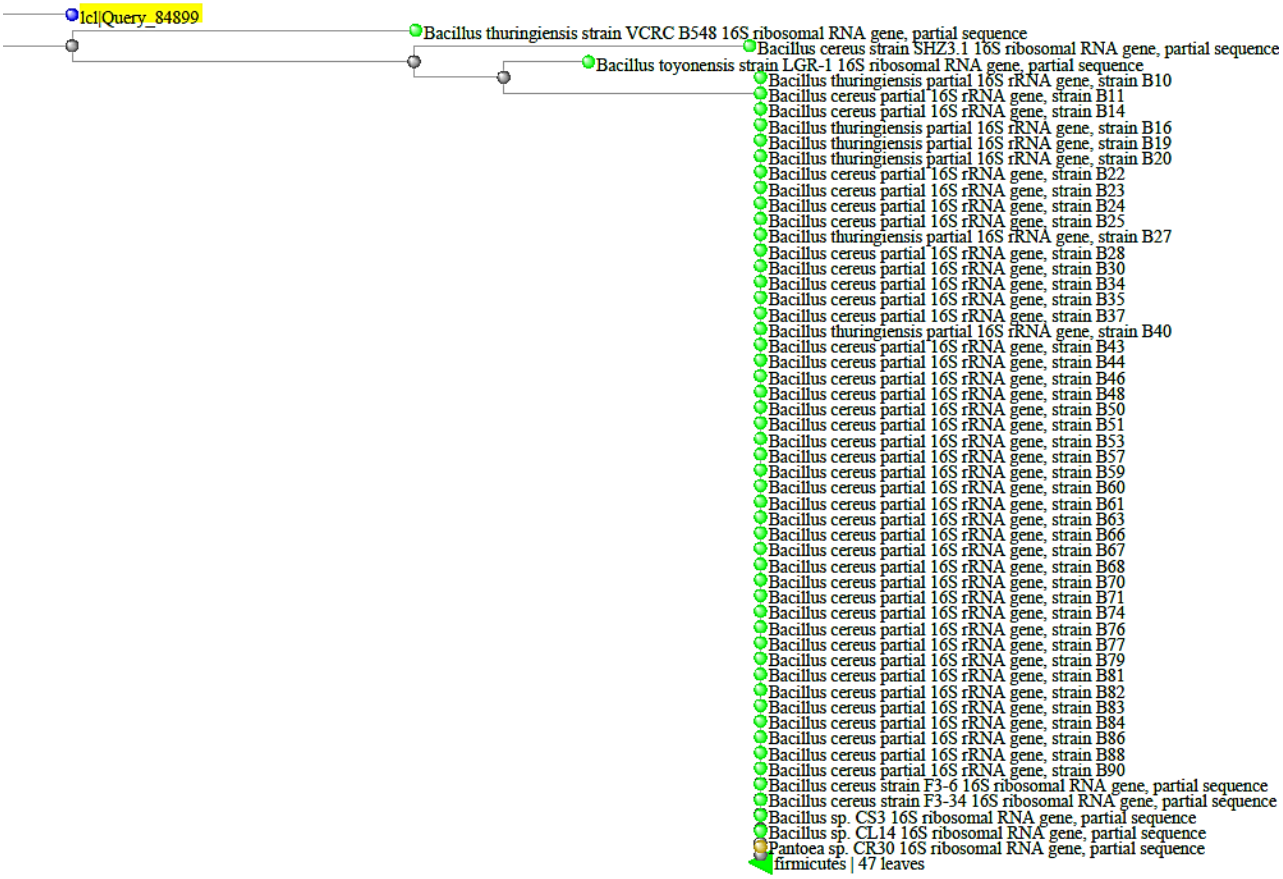
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Bacillus thuringiensis strain VCRC B548 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain SHZ3.1 16S ribosomal RNA gene, partial sequence
Bacillus toyonensis strain LGR-1 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis partial 16S rRNA gene, strain B10
Bacillus cereus partial 16S rRNA gene, strain B11
Bacillus cereus partial 16S rRNA gene, strain B14
Bacillus thuringiensis partial 16S rRNA gene, strain B16
Bacillus thuringiensis partial 16S rRNA gene, strain B19
Bacillus thuringiensis partial 16S rRNA gene, strain B20
Bacillus cereus partial 16S rRNA gene, strain B22
Bacillus cereus partial 16S rRNA gene, strain B23
Bacillus cereus partial 16S rRNA gene, strain B24
Bacillus cereus partial 16S rRNA gene, strain B25
Bacillus thuringiensis partial 16S rRNA gene, strain B27
Bacillus cereus partial 16S rRNA gene, strain B28
Bacillus cereus partial 16S rRNA gene, strain B30
Bacillus cereus partial 16S rRNA gene, strain B34
Bacillus cereus partial 16S rRNA gene, strain B35
Bacillus cereus partial 16S rRNA gene, strain B37
Bacillus thuringiensis partial 16S rRNA gene, strain B40
Bacillus cereus partial 16S rRNA gene, strain B43
Bacillus cereus partial 16S rRNA gene, strain B44
Bacillus cereus partial 16S rRNA gene, strain B46
Bacillus cereus partial 16S rRNA gene, strain B48
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Bacillus cereus partial 16S rRNA gene, strain B59
Bacillus cereus partial 16S rRNA gene, strain B60
Bacillus cereus partial 16S rRNA gene, strain B61
Bacillus cereus partial 16S rRNA gene, strain B63
Bacillus cereus partial 16S rRNA gene, strain B66
Bacillus cereus partial 16S rRNA gene, strain B67
Bacillus cereus partial 16S rRNA gene, strain B68
Bacillus cereus partial 16S rRNA gene, strain B70
Bacillus cereus partial 16S rRNA gene, strain B71
Bacillus cereus partial 16S rRNA gene, strain B74
Bacillus cereus partial 16S rRNA gene, strain B76
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Bacillus cereus partial 16S rRNA gene, strain B79
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Bacillus cereus partial 16S rRNA gene, strain B83
Bacillus cereus partial 16S rRNA gene, strain B84
Bacillus cereus partial 16S rRNA gene, strain B86
Bacillus cereus partial 16S rRNA gene, strain B88
Bacillus cereus partial 16S rRNA gene, strain B90
Bacillus cereus strain F3-6 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain F3-34 16S ribosomal RNA gene, partial sequence
Bacillus sp. CS3 16S ribosomal RNA gene, partial sequence
Bacillus sp. CL14 16S ribosomal RNA gene, partial sequence
Pantoea sp. CR30 16S ribosomal RNA gene, partial sequence
firmicutes | 47 leaves

Bacillus altitudinis KT758615.1

Bacillus altitudinis strain HQB822 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT758615.1| **Length:** 1111 **Number of Matches:** 1

Range 1: 27 to 1077 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1817 bits(2014)	0.0	1036/1052(98%)	3/1052(0%)	Plus/Plus

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Sbjct  27    CCGGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGAT  86

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Sbjct  87    AACTCCGGGAAACCGGAGCTAATACCGGATAGTTCCTTGAACCGCATGGTTCAAGGATGA  146

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Sbjct  147   AAGACGGTTTCGGCTGTCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGT  206

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Sbjct  207   AACGGCTCACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGA  266

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Sbjct  267   CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGA  326

Query  301   AAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTG  360
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Sbjct  327   AAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTG  386

Query  361   TTAGGGAAGAACAAGTGCAAGAGTAACTGCTTGCACCTTGACGGTACCTAACCAGAAAGC  420
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Sbjct  387   TTAGGGAAGAACAAGTGCAAGAGTAACTGCTTGCACCTTGACGGTACCTAACCAGAAAGC  446

Query  421   CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  480
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Sbjct  447   CACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAAT  506

Query  481   TATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCA  540
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Sbjct  627   CGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTG  686

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Sbjct  927   TTACCAGGTC-TGACATCCTCTGACACCCTAGAGATAGGGCTTTCCCTTCGGGGACAGAG  985

Query  960   TGACAGGGGGGCATGGTTGTCGTGAGCTCGGGTCGGGAAATGTTGGGTTAAGTCCCGCAC  1019
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Sbjct  986   TGACAGTGGTGCATGGTTGTCGTCAGCTCTGGTCGTGAGATGTTGGGTTAAGTCCCGCAC  1045

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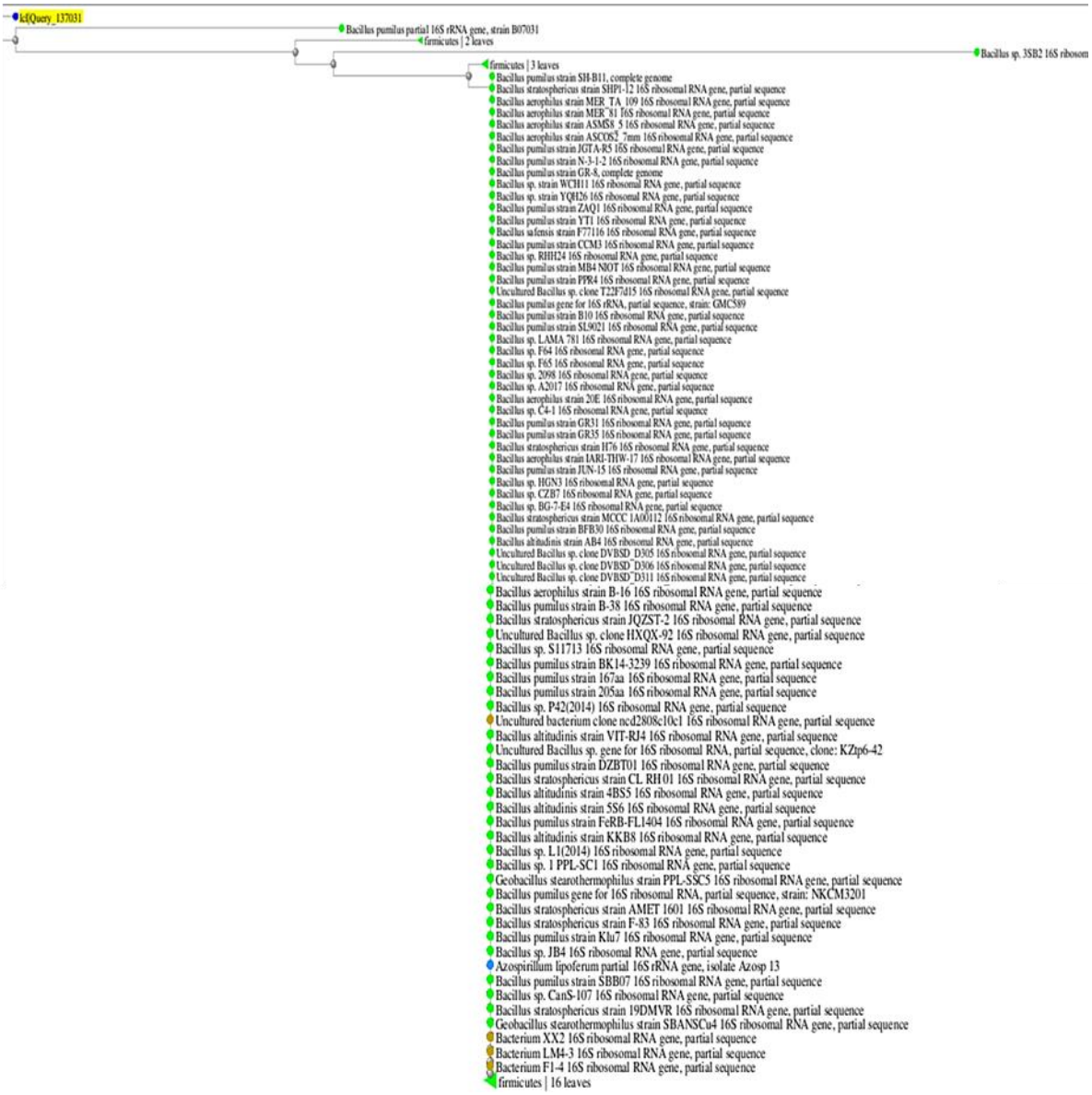
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Bacillus pumilus partial 16S rRNA gene, strain B07031
firmicutes | 2 leaves
Bacillus sp. 3SB2 16S ribosom
firmicutes | 3 leaves
Bacillus pumilus strain SH-B11, complete genome
Bacillus stratosphericus strain SHP1-12 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain MER_TA_109 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain MER_81 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain ASMS8_5 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain ASCOS2_7mm 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain IGTA-R5 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain N-3-1-2 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain GR-8, complete genome
Bacillus sp. strain WCH11 16S ribosomal RNA gene, partial sequence
Bacillus sp. strain YQH26 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain ZAQ1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain YT1 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain F77116 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain CCM3 16S ribosomal RNA gene, partial sequence
Bacillus sp. RIIH24 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain MB4 NIOT 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain PPR4 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone T22F7d15 16S ribosomal RNA gene, partial sequence
Bacillus pumilus gene for 16S rRNA, partial sequence, strain: GMC589
Bacillus pumilus strain B10 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SL9021 16S ribosomal RNA gene, partial sequence
Bacillus sp. LAMA 781 16S ribosomal RNA gene, partial sequence
Bacillus sp. F64 16S ribosomal RNA gene, partial sequence
Bacillus sp. F65 16S ribosomal RNA gene, partial sequence
Bacillus sp. 2098 16S ribosomal RNA gene, partial sequence
Bacillus sp. A2017 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain 20E 16S ribosomal RNA gene, partial sequence
Bacillus sp. C4-1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain GR31 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain GR35 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain H76 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain IARI-THW-17 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain JUN-15 16S ribosomal RNA gene, partial sequence
Bacillus sp. HGN3 16S ribosomal RNA gene, partial sequence
Bacillus sp. CZB7 16S ribosomal RNA gene, partial sequence
Bacillus sp. BG-7-E4 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain MCCC 1A00112 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain BFB30 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain AB4 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone DVBSD_D305 16S ribosomal RNA gene, partial sequence
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Uncultured Bacillus sp. clone DVBSD_D311 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain B-16 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain B-38 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain JQZST-2 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone HXQX-92 16S ribosomal RNA gene, partial sequence
Bacillus sp. S11713 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain BK14-3239 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain 167aa 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain 205aa 16S ribosomal RNA gene, partial sequence
Bacillus sp. P42(2014) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2808c10c1 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain VIT-RJ4 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, clone: KZtp6-42
Bacillus pumilus strain DZBT01 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain CL_RH01 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain 4BS5 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain 5S6 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain FeRB-FL1404 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain KKB8 16S ribosomal RNA gene, partial sequence
Bacillus sp. L1(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. 1 PPL-SC1 16S ribosomal RNA gene, partial sequence
Geobacillus stearothermophilus strain PPL-SSC5 16S ribosomal RNA gene, partial sequence
Bacillus pumilus gene for 16S ribosomal RNA, partial sequence, strain: NKCM3201
Bacillus stratosphericus strain AMET 1601 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain F-83 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain Klu7 16S ribosomal RNA gene, partial sequence
Bacillus sp. JB4 16S ribosomal RNA gene, partial sequence
Azospirillum lipoferum partial 16S rRNA gene, isolate Azosp 13
Bacillus pumilus strain SBB07 16S ribosomal RNA gene, partial sequence
Bacillus sp. CanS-107 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain 19DMVR 16S ribosomal RNA gene, partial sequence
Geobacillus stearothermophilus strain SBANSCu4 16S ribosomal RNA gene, partial sequence
Bacterium XX2 16S ribosomal RNA gene, partial sequence
Bacterium LM4-3 16S ribosomal RNA gene, partial sequence
Bacterium F1-4 16S ribosomal RNA gene, partial sequence
firmicutes | 16 leaves

Bacillus pumilus KP322017.1

Bacillus pumilus strain MK16 16S ribosomal RNA gene, partial sequence
Sequence ID: gb|KP322017.1| **Length:** 1469 **Number of Matches:** 1

Range 1: 64 to 1120 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1799 bits(1994)	0.0	1038/1057(98%)	6/1057(0%)	Plus/Plus

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Sbjct  64    CCCGGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGA  123

Query  61    TAACTCCGGGAAACCGGAGCTAATACCGGATAGTTCCTTGAACCGCATGGTTCAAGGATG  120
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Sbjct  184   AAAGACGGTTTCGGCTGTCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGGGG  243

Query  181   TAATGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGG  240
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Sbjct  484   CCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAA  543

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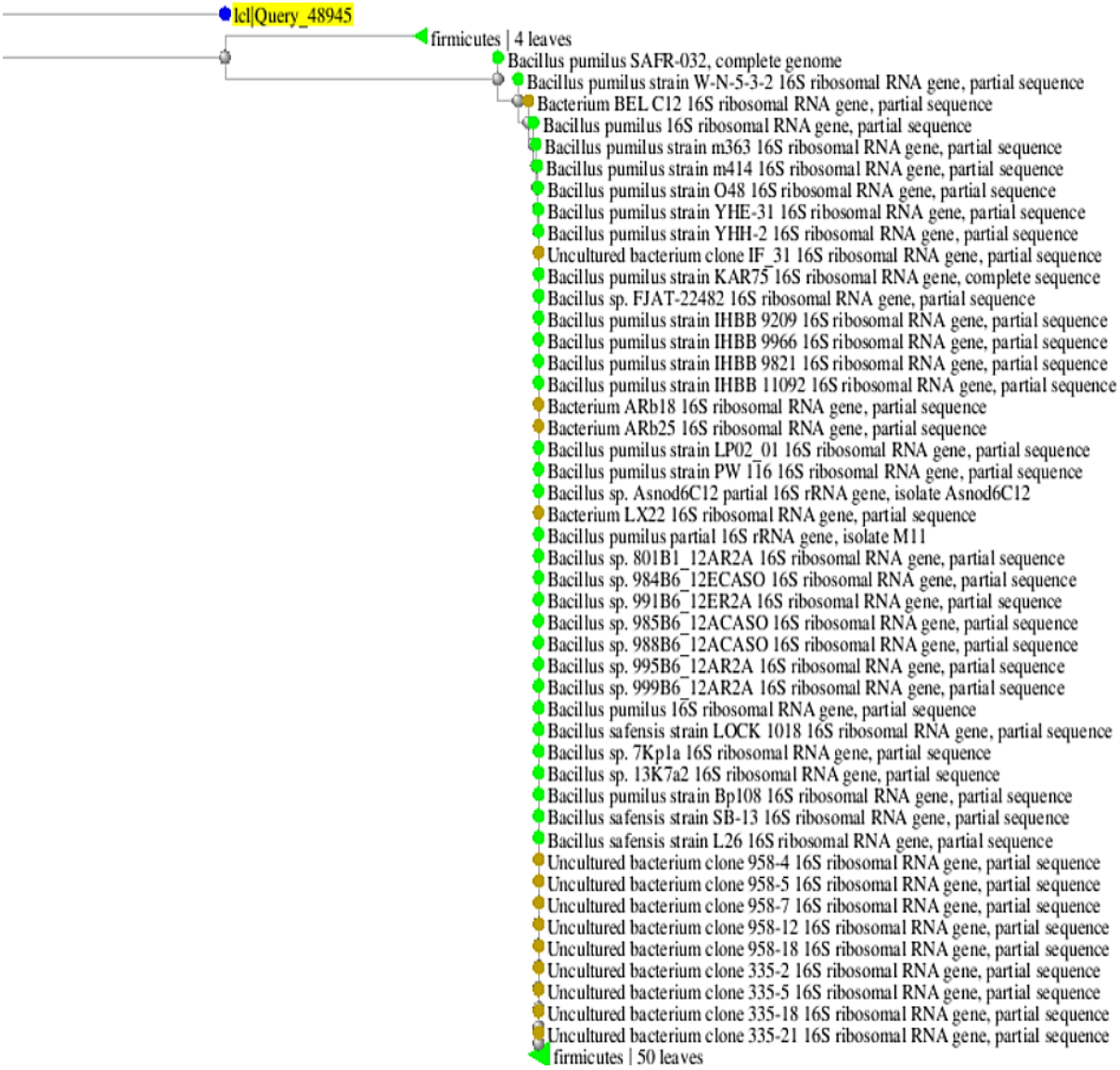
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firmicutes | 4 leaves
Bacillus pumilus SAFR-032, complete genome
Bacillus pumilus strain W-N-5-3-2 16S ribosomal RNA gene, partial sequence
Bacterium BEL C12 16S ribosomal RNA gene, partial sequence
Bacillus pumilus 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain m363 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain m414 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain O48 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain YHE-31 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain YHH-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone IF_31 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain KAR75 16S ribosomal RNA gene, complete sequence
Bacillus sp. FJAT-22482 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain IHBB 9209 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain IHBB 9966 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain IHBB 9821 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain IHBB 11092 16S ribosomal RNA gene, partial sequence
Bacterium ARb18 16S ribosomal RNA gene, partial sequence
Bacterium ARb25 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain LP02_01 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain PW 116 16S ribosomal RNA gene, partial sequence
Bacillus sp. Asnod6C12 partial 16S rRNA gene, isolate Asnod6C12
Bacterium LX22 16S ribosomal RNA gene, partial sequence
Bacillus pumilus partial 16S rRNA gene, isolate M11
Bacillus sp. 801B1_12AR2A 16S ribosomal RNA gene, partial sequence
Bacillus sp. 984B6_12ECASO 16S ribosomal RNA gene, partial sequence
Bacillus sp. 991B6_12ER2A 16S ribosomal RNA gene, partial sequence
Bacillus sp. 985B6_12ACASO 16S ribosomal RNA gene, partial sequence
Bacillus sp. 988B6_12ACASO 16S ribosomal RNA gene, partial sequence
Bacillus sp. 995B6_12AR2A 16S ribosomal RNA gene, partial sequence
Bacillus sp. 999B6_12AR2A 16S ribosomal RNA gene, partial sequence
Bacillus pumilus 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain LOCK 1018 16S ribosomal RNA gene, partial sequence
Bacillus sp. 7Kp1a 16S ribosomal RNA gene, partial sequence
Bacillus sp. 13K7a2 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain Bp108 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain SB-13 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain L26 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-12 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-21 16S ribosomal RNA gene, partial sequence
firmicutes | 50 leaves

Bacillus stratosphericus KJ672335.1

Bacillus stratosphericus strain MUGA150 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ672335.1| **Length:** 1404 **Number of Matches:** 1

Range 1: 326 to 1371 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1781 bits(1974)	0.0	1026/1046(98%)	7/1046(0%)	Plus/Minus

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Query  1     TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTG  60
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Sbjct  1371  TCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTG  1312

Query  61    ATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACT  120
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Sbjct  1311  ATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACT  1252

Query  121   GAGAACAGATTTGTGGGATTGGCTAAACCTTGCGGTCTCGCAGCCCTTTGTTCTGTCCAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1251  GAGAACAGATTTGTGGGATTGGCTAAACCTTGCGGTCTCGCAGCCCTTTGTTCTGTCCAT  1192

Query  181   TGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1191  TGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT  1132

Query  241   CCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGAT  300
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Sbjct  1131  CCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGAT  1072

Query  301   CAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC  360
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Sbjct  1071  CAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAAC  1012

Query  361   CATGCACCACCTGTCACTCTGTCCCCGAAGGGAAAGTCCTATCTCTAGGGTTGTCAGAGG  420
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  1011  CATGCACCACCTGTCACTCTGTCCCCGAAGGGAAAGCCCTATCTCTAGGGTTGTCAGAGG  952

Query  421   ATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  951   ATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCT  892

Query  481   TGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  891   TGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGA  832

Query  541   GTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCAT  600
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Sbjct  831   GTGCTTAATGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCAT  772

Query  601   CGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  771   CGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCT  712

Query  661   CAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACG  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  711   CAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACG  652

Query  721   CATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTTCCCAGTTTC  780
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Sbjct  651   CATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTTCCCAGTTTC  592

Query  781   CAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACCGCCTGCGA  840
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Sbjct  591   CAATGACCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGA  532

Query  841   GCCCTTTACGCCCGATAATTCCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCT  900
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531   GCCCTTTACGCCCAATAATTCCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCT  472

Query  901   GGCACGTATTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGGGCAAGCAGTTACTCTT  960
             |||||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  471   GGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCAAGCAGTTACTCTT  412

Query  961   GCACTTGTTCTTCCCTA--CACAAAACTTTACAATCC-AAAACCTTCATCCCTC-CGCGG  1016
             ||||||||||||||||    ||| | |||||| |||| |||||||||||| ||| |||||
Sbjct  411   GCACTTGTTCTTCCCTAACAACAGAGCTTTACGATCCGAAAACCTTCATCACTCACGCGG  352

Query  1017  CGTTGCT-CGTCAAA--TTCCTCCAT  1039
             ||||||| ||||| |   ||| |||||
Sbjct  351   CGTTGCTCCGTCAGACTTTCGTCCAT  326
```


Bacillus pumilus strain ku-bf1 genome
lcl|Query_134117
Bacillus aerophilus strain MER_18 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus pumilus strain CTO-05 16S ribosomal RNA gene, partial sequence
firmicutes | 7 leaves
Bacterium ST3(2015) strain ST3 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain IHBB 11116 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain MD-A19 16S ribosomal RNA gene, partial sequence
Endophylic bacterium SV686 16S ribosomal RNA gene, partial sequence
Bacillus sp. UYFA152 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK63 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK45 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK21 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain FMDD_3 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain DB9-2 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain W-N-5-1-1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SH-B11, complete genome
Uncultured bacterium clone 958-6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-2 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain NS-31 16S ribosomal RNA gene, partial sequence
Bacillus sp. 16Kp3 16S ribosomal RNA gene, partial sequence
Bacillus sp. 8K15a 16S ribosomal RNA gene, partial sequence
Bacillus sp. 24bKB3 16S ribosomal RNA gene, partial sequence
Bacillus sp. 21K5e 16S ribosomal RNA gene, partial sequence
Bacillus sp. 11K19 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain LSR9.1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus partial 16S rRNA gene, strain GRC, isolate 20
Bacillus pumilus strain CRh18 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain CL19 16S ribosomal RNA gene, partial sequence
Bacillus aerius strain CL4 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain CL3 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus partial 16S rRNA gene, strain B89
Bacillus aerius strain SBANSCu8 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain CanR-21 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain RLC_11 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain RSC_05 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain RHM_109 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain RHM_104 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain Bacteria VII 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain ASR-31 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain IHBB 11166 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain IHBB 9411 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain SBB27 16S ribosomal RNA gene, partial sequence
Bacillus pumilus 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain KHC2d 16S ribosomal RNA gene, partial sequence
Bacterium M1(2015b) strain M1 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain KP092r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Q31 16S ribosomal RNA gene, partial sequence
Bacillus sp. Q11 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain HN-8 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain n11 16S ribosomal RNA gene, partial sequence
Bacillus sp. CICC 23870 16S ribosomal RNA gene, partial sequence
Bacillus sp. WS(2015) 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain LKM-PD 16S ribosomal RNA gene, partial sequence
Endophylic bacterium SV887 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone YXY-11 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain KNUSC1056 16S ribosomal RNA gene, partial sequence
Bacillus pumilus isolate YXY-11 16S ribosomal RNA gene, partial sequence
Bacillus sp. JXRH25 16S ribosomal RNA gene, partial sequence
Bacillus sp. JXL24 16S ribosomal RNA gene, partial sequence
Bacillus sp. DB14733 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. clone DDGI11 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain BS25 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain BS19 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain LGR-6 16S ribosomal RNA gene, partial sequence
Bacillus aerius strain LGS-1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain PPL-SC14 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain GS-305 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain GW-605 16S ribosomal RNA gene, partial sequence
Bacillus sp. JBS-9 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Bf25
Bacillus altitudinis strain IHB B 15457 16S ribosomal RNA gene, partial sequence
Bacillus aerius strain LLS.IE(B)-1 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain LP31_R11 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain BGZ-9 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain BCX-57 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain LAMA 1175 16S ribosomal RNA gene, partial sequence
Bacillus stratosphericus strain LAMA 1114 16S ribosomal RNA gene, partial sequence
Bacillus sp. LTW29 16S ribosomal RNA gene, partial sequence
Bacillus sp. WP-A-6 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb58 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
Bacillus sp. hb117 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb49 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain -Y15 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain JK-SX001 16S ribosomal RNA gene, partial sequence
Bacillus aerophilus strain Van2 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus sp. WP-A-3 16S ribosomal RNA gene, partial sequence
0.0006

Bacillus weihenstephanensis KC527665.1

Bacillus weihenstephanensis strain A2-25c-6b 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KC527665.1| **Length:** 1252 **Number of Matches:** 1

Range 1: 161 to 1197 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1750 bits(1940)	0.0	1016/1038(98%)	7/1038(0%)	Plus/Minus

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Query  1     CAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCA  60
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Sbjct  1197  CAAACTCTCG-GGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCA  1139

Query  61    TGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  TGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCC  1079

Query  121   GAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1078  GAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCG  1019

Query  181   TCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  TCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCC  959

Query  241   ACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACT  300
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Sbjct  958   ACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACT  899

Query  301   AAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898   AAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACG  839

Query  361   ACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGGTTTTC  420
             |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  838   ACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCTCTATCTCTAGAGTTTTC  779

Query  421   AGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCA  480
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Sbjct  778   AGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCA  719

Query  481   CCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAG  540
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Sbjct  718   CCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAG  659

Query  541   GCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  658   GCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCA  599

Query  601   CTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCG  660
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Sbjct  598   CTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCG  539

Query  661   CGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCT  720
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Sbjct  538   CGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCT  479

Query  721   CTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCA  780
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Sbjct  478   CTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCA  419

Query  781   GTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAAACTTAA-AAACCACC  839
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Sbjct  418   GTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACC  359

Query  840   TGCGCGCGCTTTACGCCCAATAATTCCGGA-AACGCTTGCCACCTACGTATTACCGCGGC  898
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  358   TGCGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGC  299

Query  899   TGCTGGCACGTAATTAGCCG-GGCTTTCTGGTTAGGTACCGTCAGGGGCCAGNTTATTCA  957
             |||||||||||| ||||||| |||||||||||||||||||||||| ||||| |||||||
Sbjct  298   TGCTGGCACGTAGTTAGCCGTGGCTTTCTGGTTAGGTACCGTCAGGTGCCAGCTTATTCA  239

Query  958   ACTAGCATTTGTTCTTCCT-ACACAAATTTTAC-AACCGAAGCTTCATCACTC-CNCGCG  1014
             ||||||| |||||||||| ||||| | ||||| | |||||||||||||||| | ||||
Sbjct  238   ACTAGCACTTGTTCTTCCTAACACAGAGTTTACGACCCGAAGCTTCATCACTCACGCGCG  179

Query  1015  TGCCCGTCAAAATTCCTC  1032
             ||| ||||| | ||| ||
Sbjct  178   TGCTCGTCAGACTTCGTC  161
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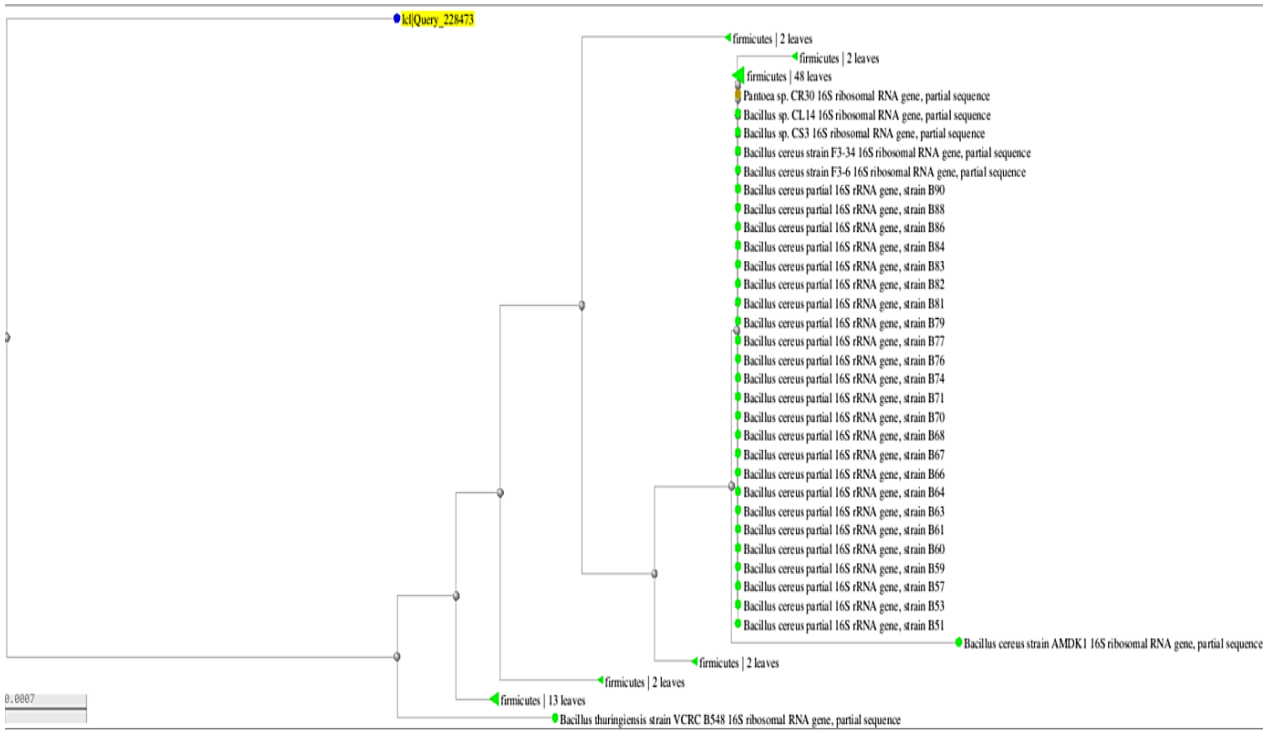
kl|Query_228473
firmicutes | 2 leaves
firmicutes | 2 leaves
firmicutes | 48 leaves
Pantoea sp. CR30 16S ribosomal RNA gene, partial sequence
Bacillus sp. CL14 16S ribosomal RNA gene, partial sequence
Bacillus sp. CS3 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain F3-34 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain F3-6 16S ribosomal RNA gene, partial sequence
Bacillus cereus partial 16S rRNA gene, strain B90
Bacillus cereus partial 16S rRNA gene, strain B88
Bacillus cereus partial 16S rRNA gene, strain B86
Bacillus cereus partial 16S rRNA gene, strain B84
Bacillus cereus partial 16S rRNA gene, strain B83
Bacillus cereus partial 16S rRNA gene, strain B82
Bacillus cereus partial 16S rRNA gene, strain B81
Bacillus cereus partial 16S rRNA gene, strain B79
Bacillus cereus partial 16S rRNA gene, strain B77
Bacillus cereus partial 16S rRNA gene, strain B76
Bacillus cereus partial 16S rRNA gene, strain B74
Bacillus cereus partial 16S rRNA gene, strain B71
Bacillus cereus partial 16S rRNA gene, strain B70
Bacillus cereus partial 16S rRNA gene, strain B68
Bacillus cereus partial 16S rRNA gene, strain B67
Bacillus cereus partial 16S rRNA gene, strain B66
Bacillus cereus partial 16S rRNA gene, strain B64
Bacillus cereus partial 16S rRNA gene, strain B63
Bacillus cereus partial 16S rRNA gene, strain B61
Bacillus cereus partial 16S rRNA gene, strain B60
Bacillus cereus partial 16S rRNA gene, strain B59
Bacillus cereus partial 16S rRNA gene, strain B57
Bacillus cereus partial 16S rRNA gene, strain B53
Bacillus cereus partial 16S rRNA gene, strain B51
Bacillus cereus strain AMDK1 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
firmicutes | 2 leaves
firmicutes | 13 leaves
Bacillus thuringiensis strain VCRC B548 16S ribosomal RNA gene, partial sequence
0.0007

Acinetobacter lofwii KT387352.1

Acinetobacter lwoffii strain CL_102 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT387352.1| **Length:** 1437 **Number of Matches:** 1

Range 1: 425 to 1356 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1640 bits(1818)	0.0	923/932(99%)	0/932(0%)	Plus/Minus

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Query  1     GTACAAGGCCCGGGAACGTATTCACCGCGGCATTCTGATCCGCGATTACTAGCGATTCCG  60
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Sbjct  1356  GTACAAGGCCCGGGAACGTATTCACCGCGGCATTCTGATCCGCGATTACTAGCGATTCCG  1297

Query  61    ACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTTTGAGATTAGC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1296  ACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTTTGAGATTAGC  1237

Query  121   ATCCTCTCGCGAGGTAGCAACCCTTTGTACCGACCATTGTAGCACGTGTGTAGCCCTGGT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1236  ATCCTCTCGCGAGGTAGCAACCCTTTGTACCGACCATTGTAGCACGTGTGTAGCCCTGGT  1177

Query  181   CGTAAGGGCCATGATGACTTGACGTCGTCCCCGCCTTCCTCCAGTTTGTCACTGGCAGTA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1176  CGTAAGGGCCATGATGACTTGACGTCGTCCCCGCCTTCCTCCAGTTTGTCACTGGCAGTA  1117

Query  241   TCCTTAAAGTTCCCGGCTTAACCCGCTGGCAAATAAGGAAAAGGGTTGCGCTCGTTGCGG  300
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Sbjct  1116  TCCTTAAAGTTCCCGGCTTAACCCGCTGGCAAATAAGGAAAAGGGTTGCGCTCGTTGCGG  1057

Query  301   GACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTATGTAAG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1056  GACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTATGTAAG  997

Query  361   TTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTTACTATGTCAAGACCAGGTAAGGTT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  996   TTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTTACTATGTCAAGACCAGGTAAGGTT  937

Query  421   CTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  936   CTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTC  877

Query  481   ATTTGAGTTTTAGTCTTGCGACCGTACTCCCCAGGCGGTCTACTTATCGCGTTAGCTGCG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  876   ATTTGAGTTTTAGTCTTGCGACCGTACTCCCCAGGCGGTCTACTTATCGCGTTAGCTGCG  817

Query  541   CCACTAAAGCCTCAAAGGCCCCAACGGCTAGTAGACATCGTTTACGGCATGGACTACCAG  600
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Sbjct  456   TTCTGCGAGTAACGTCCACTATCCAAGAGTAT  425
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lcl|Query_4479
Uncultured bacterium clone A-38 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain JCM 6840 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. JUN-14 16S ribosomal RNA gene, partial sequence
Gamma proteobacterium F3_a5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone J12
Prolinoborus fasciculus strain MB-11 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MG-3 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MR-13 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MR-81 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 263ZG5 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WG-70 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WG-93 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WR-168 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WB-203 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WL-242 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WTB-120 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AM-72 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain TB-142 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AB-185 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. LHG-tBW4 partial 16S rRNA gene, strain LHG-tBW4
Bacillus methylotrophicus strain 262XY6 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain M0209 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MTB-4-1 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MTA-4 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 263AY1 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain HA 522 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone XJDN-640 16S ribosomal RNA gene, partial sequence
Bacterium N2-3 16S ribosomal RNA gene, partial sequence
Endophytic bacterium SV900 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain SBB32 16S ribosomal RNA gene, partial sequence
Bacterium JNKLA9 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WD206 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain LAHP2-7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-19 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. 11K17 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain CL_102 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WD224 16S ribosomal RNA gene, partial sequence
Uncultured Acinetobacter sp. clone TCCC 11167 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain IHBB 9208 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. Sn-19 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone Bac3B100 small subunit ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MTA-33 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MTA-2 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 2A 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. Tibet-YD4820-5 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. LHG-2BW3 partial 16S rRNA gene, strain LHG-2BW3
Acinetobacter lwoffii strain AB-207 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AR-155 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain TB-128 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AL-11 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WR-169 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WL-228 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WL-199 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WM-50 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WG-92 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 265ZG8 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. Cai-b1 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain ML-21 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MB-14 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MTA-24-1 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MTA-34-1 16S ribosomal RNA gene, partial sequence
Gamma proteobacterium F3_a10 16S ribosomal RNA gene, partial sequence
Bacterium C50(2013) 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii partial 16S rRNA gene, strain Marseille-P786
Acinetobacter lwoffii strain T24 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WD238 16S ribosomal RNA gene, partial sequence
Bacterium ST8(2015) strain ST8 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 3R2 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain KAR20 16S ribosomal RNA gene, complete sequence
Acinetobacter lwoffii strain ZJY-778 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain SD11 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii partial 16S rRNA gene, isolate 10
Acinetobacter lwoffii strain 263AY7 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WR-139 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MTB-12 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain ML-39 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 266XY3 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain 272XG8 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AB-204 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AR-180 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain TB-122 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain AL-23 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WR-156 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain WL-241 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WB-216-2 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WM-65 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain WG-82 16S ribosomal RNA gene, partial sequence
Acinetobacter sp. 265ZG9 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain MR-18-2 16S ribosomal RNA gene, partial sequence
Acinetobacter lwoffii strain ML-9 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MB-24 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MM-111 16S ribosomal RNA gene, partial sequence
Prolinoborus fasciculus strain MG-20 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 3 leaves
Prolinoborus fasciculus partial 16S rRNA gene, isolate 56_SP635

Bacillus licheniformis DQ071560.1

Bacillus licheniformis strain MKU 1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|DQ071560.1| **Length:** 1430 **Number of Matches:** 1

Range 1: 437 to 1388 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1701 bits(1886)	0.0	949/952(99%)	1/952(0%)	Plus/Minus

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Sbjct  1388  AACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATG  1329

Query  61    CTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGA  120
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Sbjct  1328  CTGATCCGCGATTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGA  1269

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Query  241   CTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAA  300
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Query  301   GATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGAC  360
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Sbjct  1088  GATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGAC  1029

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Sbjct  968   AGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC  909

Query  481   GCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGC  540
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Query  661   CCTCAGCGTCAGTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCT  720
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Sbjct  668   ACGCATTTCACCGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTCCCCAGT  609

Query  781   TTCCAATGANCCTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACCGCCTG  840
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Query  901   CTGGCACGTAATTAGCCG-GGCTTTCTGGTTAGGTACCGTCAAGGTACCGCC  951
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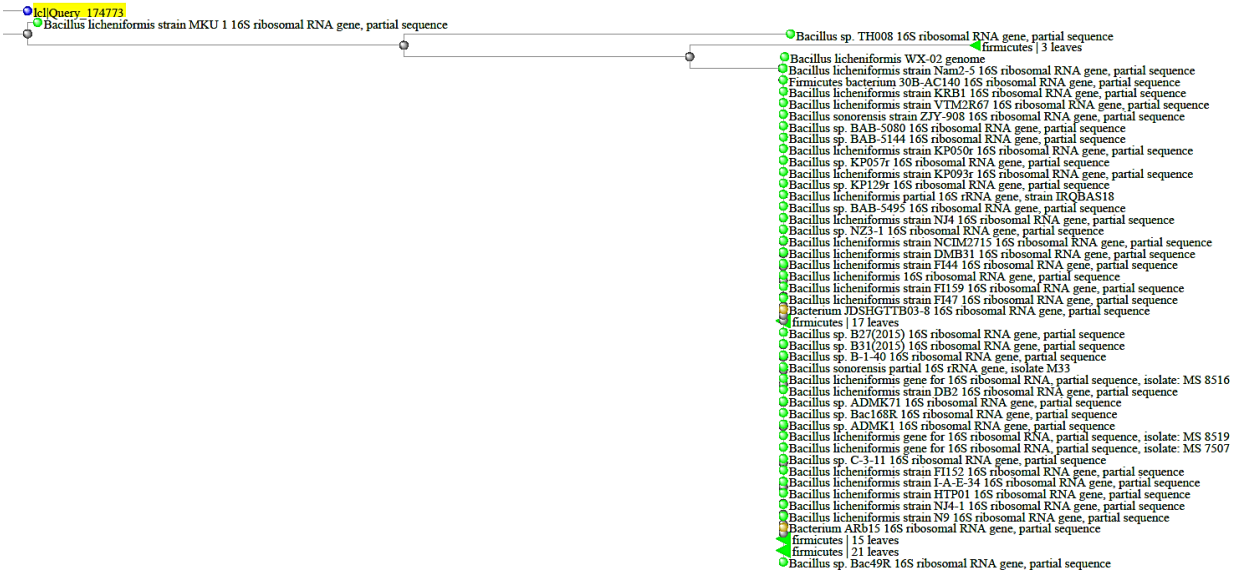
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Bacillus licheniformis strain MKU 1 16S ribosomal RNA gene, partial sequence
Bacillus sp. TH008 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Bacillus licheniformis WX-02 genome
Bacillus licheniformis strain Nam2-5 16S ribosomal RNA gene, partial sequence
Firmicutes bacterium 30B-AC140 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KRB1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain VTM2R67 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain ZJY-908 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5080 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5144 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP050r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP057r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP093r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP129r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS18
Bacillus sp. BAB-5495 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NJ4 16S ribosomal RNA gene, partial sequence
Bacillus sp. NZ3-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NCIM2715 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain DMB31 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI44 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI159 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI47 16S ribosomal RNA gene, partial sequence
Bacterium JDSHGTTB03-8 16S ribosomal RNA gene, partial sequence
firmicutes | 17 leaves
Bacillus sp. B27(2015) 16S ribosomal RNA gene, partial sequence
Bacillus sp. B31(2015) 16S ribosomal RNA gene, partial sequence
Bacillus sp. B-1-40 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis partial 16S rRNA gene, isolate M33
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 8516
Bacillus licheniformis strain DB2 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK71 16S ribosomal RNA gene, partial sequence
Bacillus sp. Bac168R 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 8519
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 7507
Bacillus sp. C-3-11 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI152 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain I-A-E-34 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain HTP01 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NJ4-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain N9 16S ribosomal RNA gene, partial sequence
Bacterium ARb15 16S ribosomal RNA gene, partial sequence
firmicutes | 15 leaves
firmicutes | 21 leaves
Bacillus sp. Bac49R 16S ribosomal RNA gene, partial sequence

Bacillus megaterium KU550043.1

Bacillus megaterium strain EB-238 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KU550043.1| **Length:** 1406 **Number of Matches:** 1

Range 1: 395 to 1361 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1721 bits(1908)	0.0	962/967(99%)	0/967(0%)	Plus/Minus

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Query  241   TTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTAAATGCTGGCAACTAAG  300
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Sbjct  1001  ACCATGCACCACCTGTCACTCTGTCCCCCGAAGGGGAACGCTCTATCTCTAGAGTTGTCA  942

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Query  961   TCTTGTA  967
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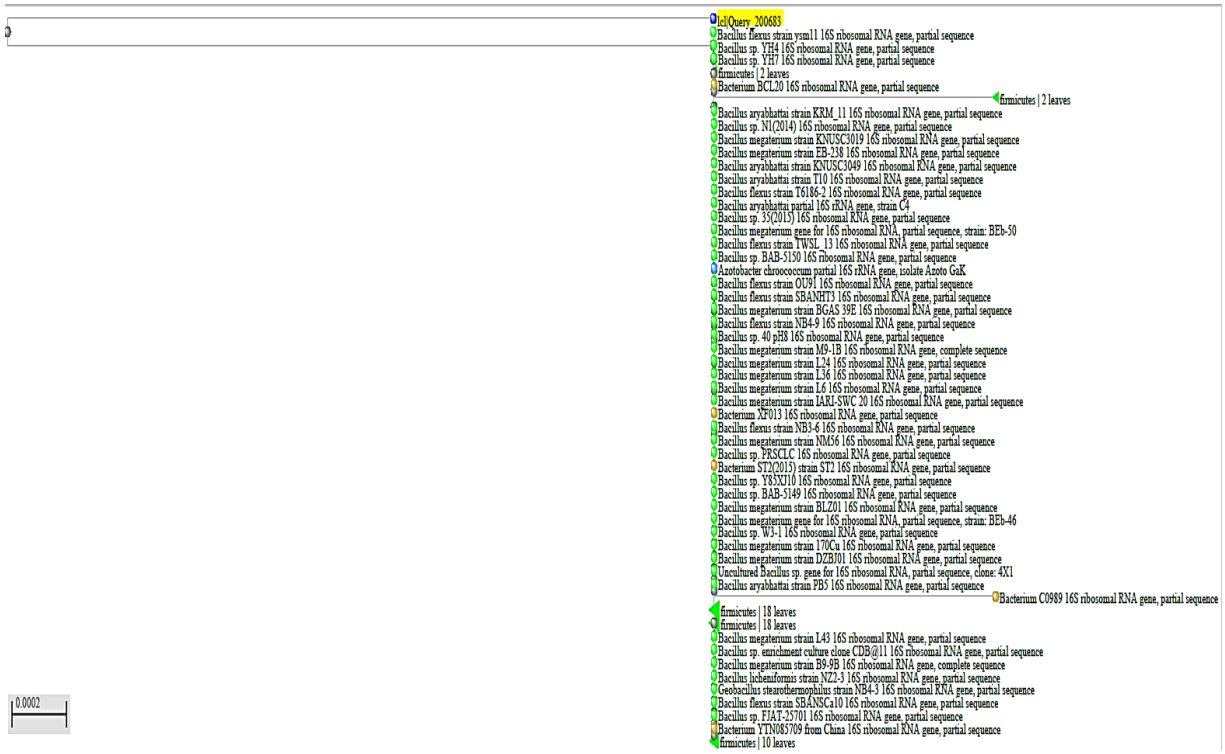
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Bacillus sp. YH4 16S ribosomal RNA gene, partial sequence
Bacillus sp. YH7 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacterium BCL20 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus aryabhattai strain KRM_11 16S ribosomal RNA gene, partial sequence
Bacillus sp. N1(2014) 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain KNUSC3019 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain EB-238 16S ribosomal RNA gene, partial sequence
Bacillus aryabhattai strain KNUSC3049 16S ribosomal RNA gene, partial sequence
Bacillus aryabhattai strain T10 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain T6186-2 16S ribosomal RNA gene, partial sequence
Bacillus aryabhattai partial 16S rRNA gene, strain C4
Bacillus sp. 35(2015) 16S ribosomal RNA gene, partial sequence
Bacillus megaterium gene for 16S ribosomal RNA, partial sequence, strain: BEb-50
Bacillus flexus strain JWSL_13 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5150 16S ribosomal RNA gene, partial sequence
Azotobacter chroococcum partial 16S rRNA gene, isolate Azoto GaK
Bacillus flexus strain OU91 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain SBANHT3 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain BGAS 39E 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain NB4-9 16S ribosomal RNA gene, partial sequence
Bacillus sp. 40 pH8 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain M9-1B 16S ribosomal RNA gene, complete sequence
Bacillus megaterium strain L24 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain L36 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain L6 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain IARI-SWC 20 16S ribosomal RNA gene, partial sequence
Bacterium XF013 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain NB3-6 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain NM56 16S ribosomal RNA gene, partial sequence
Bacillus sp. FBSCLC 16S ribosomal RNA gene, partial sequence
Bacterium ST2(2015) strain ST2 16S ribosomal RNA gene, partial sequence
Bacillus sp. Y83XJ10 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5149 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain BLZ01 16S ribosomal RNA gene, partial sequence
Bacillus megaterium gene for 16S ribosomal RNA, partial sequence, strain: BEb-46
Bacillus sp. W3-1 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain 170Cu 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain DZBJ01 16S ribosomal RNA gene, partial sequence
Uncultured Bacillus sp. gene for 16S ribosomal RNA, partial sequence, clone: 4X1
Bacillus aryabhattai strain PB5 16S ribosomal RNA gene, partial sequence
Bacterium C0989 16S ribosomal RNA gene, partial sequence
firmicutes | 18 leaves
firmicutes | 18 leaves
Bacillus megaterium strain L43 16S ribosomal RNA gene, partial sequence
Bacillus sp. enrichment culture clone CDB@11 16S ribosomal RNA gene, partial sequence
Bacillus megaterium strain B9-9B 16S ribosomal RNA gene, complete sequence
Bacillus licheniformis strain NZ2-3 16S ribosomal RNA gene, partial sequence
Geobacillus stearothermophilus strain NB4-3 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain SBANSCa10 16S ribosomal RNA gene, partial sequence
Bacillus sp. FJAT-25701 16S ribosomal RNA gene, partial sequence
Bacterium YTN085709 from China 16S ribosomal RNA gene, partial sequence
firmicutes | 10 leaves
0.0002

Staphylococcus succiuns **KJ888125.1**

Staphylococcus succinus strain MI-6 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ888125.1| **Length:** 1381 **Number of Matches:** 1

Range 1: 40 to 988 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1660 bits(1840)	0.0	940/949(99%)	3/949(0%)	Plus/Plus

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Query  1    AACACGTGGGTAACCTACCTATAAGACTGGAATAACTTCGGGAAACCGGAGCTAATGCCG  60
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Sbjct  40   AACACGTGGGTAACCTACCTATAAGACTGGAATAACTTCGGGAAACCGGAGCTAATGCCG  99

Query  61   GATAACATATAGAACCGCATGGTTCTATAGTGAAAGATGGTTTTGCTATCACTTATAGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  100  GATAACATATAGAACCGCATGGTTCTATAGTGAAAGATGGTTTTGCTATCACTTATAGAT  159

Query  121  GGACCCGCGCCGTATTAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCGACGATACGTAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  160  GGACCCGCGCCGTATTAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCGACGATACGTAG  219

Query  181  CCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  220  CCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGA  279

Query  241  GGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGT  300
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Sbjct  280  GGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGT  339

Query  301  GATGAAGGTTTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAAATGCGTAAGTAACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  340  GATGAAGGTTTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAAATGCGTAAGTAACT  399

Query  361  GTGCGCATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  400  GTGCGCATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG  459

Query  421  GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  460  GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGT  519

Query  481  TTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520  TTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAA  579

Query  541  ACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  580  ACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATAT  639

Query  601  GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  640  GGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAG  699

Query  661  CGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  700  CGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAA  759

Query  721  GTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGG  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  760  GTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGG  819

Query  781  AGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  820  AGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGC  879

Query  841  ATGTGGTTTAATTCGAAGCAACGCGAAAAACCTTACC-AATCTTGACATCCTTTG-AAAC  898
            |||||||||||||||||||||||||| ||||||||| |||||||||||||||||| ||||
Sbjct  880  ATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGAAAAC  939

Query  899  TCTAAAGATAAAGCCTTCCCCTTCGGGGGA-AAAGGGACAgggggggCA  946
            |||| ||||| ||||||||||||||||||| |||| |||||| || |||
Sbjct  940  TCTAGAGATAGAGCCTTCCCCTTCGGGGGACAAAGTGACAGGTGGTGCA  988
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Staphylococcus succinus strain IARI-SL-31 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone C1_13 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain EN4 16S ribosomal RNA gene, partial sequence
lcl|Query_172339
Staphylococcus succinus subsp. succinus partial 16S rRNA gene, isolate 0911MAR22V8
Staphylococcus succinus strain AMG-D1 16S ribosomal RNA gene, complete sequence
Uncultured Staphylococcus sp. clone Gexpansi21 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. NP24 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain EM17 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain T16 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Uncultured bacterium clone nbw766g04c1 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Staphylococcus succinus strain EK2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone FB04B03
Staphylococcus succinus strain S2 16S ribosomal RNA gene, partial sequence
Staphylococcus xylosus strain T18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1178f05c1 16S ribosomal RNA gene, partial sequence
firmicutes | 3 leaves
Staphylococcus succinus strain IHB B 6872 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd980c06c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain 57A (C3P2) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw316a05c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus subsp. succinus strain M1-10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw776g02c1 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Staphylococcus sp. MT5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw312h03c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain 99A (BR46) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd128e10c1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. L5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1178f07c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain GCA867 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. M208-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw228d02c1 16S ribosomal RNA gene, partial sequence
Uncultured Firmicutes bacterium clone b5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw315g07c1 16S ribosomal RNA gene, partial sequence
Uncultured Staphylococcus sp. clone bottae10 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. TM6_3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw250g10c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain M40 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw777d08c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain 1 (C3S1) 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw316a06c1 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Uncultured bacterium clone D128_ERTV_4 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain EGY-SCC1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain NI-6 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain SV17 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus NIPHL090904/K5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw779b03c1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain JDM2_2A 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Cr5 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. 614B2_12EGalle 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Be-8 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. Be-4 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus subsp. succinus strain PK-1 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain ASW2C 16S ribosomal RNA gene, partial sequence
Staphylococcus succinus strain IARI-J-24 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd950g08c1 16S ribosomal RNA gene, partial sequence
firmicutes | 4 leaves
bacteria | 4 leaves
Staphylococcus succinus strain SI-15-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S ribosomal RNA, partial sequence, Bacterium Y
firmicutes | 4 leaves
Staphylococcus equorum subsp. equorum partial 16S rRNA gene, isolate 0312MAR
Staphylococcus gallinarum strain JDM2_3A 16S ribosomal RNA gene, partial sequen
bacteria | 17 leaves

Bacillus pumilus KU230023.1

Bacillus pumilus strain m350 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KU230023.1| **Length:** 1396 **Number of Matches:** 1

Range 1: 399 to 1340 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1663 bits(1844)	0.0	934/942(99%)	0/942(0%)	Plus/Minus

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Query  1     TGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGA  60
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Sbjct  1340  TGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGA  1281

Query  61    TTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACTGAGAACAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1280  TTACTAGCGATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACTGAGAACAG  1221

Query  121   ATTTATGGGATTGGCTAAACCTTGCGGTCTTGCAGCCCTTTGTTCTGTCCATTGTAGCAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1220  ATTTATGGGATTGGCTAAACCTTGCGGTCTTGCAGCCCTTTGTTCTGTCCATTGTAGCAC  1161

Query  181   GTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1160  GTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGT  1101

Query  241   TTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGATCAAGGGTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1100  TTGTCACCGGCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGATCAAGGGTT  1041

Query  301   GCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  GCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACC  981

Query  361   ACCTGTCACTCTGTCCCCGAAGGGAAAGCCCTATCTCTAGGGTTGTCAGAGGATGTCAAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   ACCTGTCACTCTGTCCCCGAAGGGAAAGCCCTATCTCTAGGGTTGTCAGAGGATGTCAAG  921

Query  421   ACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   ACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGG  861

Query  481   CCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  860   CCCCCGTCAATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAA  801

Query  541   TGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGTTTACG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   TGCGTTAGCTGCAGCACTAAGGGGCGGAAACCCCCTAACACTTAGCACTCATCGTTTACG  741

Query  601   GCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCTCAGCGTCA  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   GCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCTCAGCGTCA  681

Query  661   GTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCAC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   GTTACAGACCAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCAC  621

Query  721   CGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTTCCCAGTTTCCAATGACC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   CGCTACACGTGGAATTCCACTCTCCTCTTCTGCACTCAAGTTTCCCAGTTTCCAATGACC  561

Query  781   CTCCCCGGTTGAGCCGGGGGCTTTCACATCAAACTTAAAAAACCGCCTGCGAGCCCTTTA  840
             |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Sbjct  560   CTCCCCGGTTGAGCCGGGGGCTTTCACATCAGACTTAAGAAACCGCCTGCGAGCCCTTTA  501

Query  841   CGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAA  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   CGCCCAATAATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAG  441

Query  901   TTAGCCGGGGCTTTCTGGGTTAGTACCGTCAAGGGGCGAGCA  942
             ||||||| |||||||||| |  |||||||||||| |||||||
Sbjct  440   TTAGCCGTGGCTTTCTGGTTAGGTACCGTCAAGGTGCGAGCA  399
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kfQuery_52705
Bacillus sp. WMR1 16S ribosomal RNA gene, partial sequence
Bacillus sp. N17(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. SW-12 16S ribosomal RNA gene, partial
Bacillus sp. G121 16S ribosomal RNA gene, partial sequence
Bacillus sp. M403(2014) 16S ribosomal RNA gene, partial sequence
Bacillus sp. M408 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain AS02 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain C11 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain GA-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. CT 7-03 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain KP1 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain YR1 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain B31 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain E-1-1-1 16S ribosomal RNA gene, partial sequence
Bacillus sp. RKAT-0008 partial 16S rRNA gene, isolate RKAT-0008
Bacillus sp. BAB-5103 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5275 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain I4 16S ribosomal RNA gene, partial sequence
Bacillus sp. FJAT-22379 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain IHBB 9177 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain ASR-35 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain C1C3702 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SBANHCa15 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain UBT4 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain CR33 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain BS131 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain L26 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-21 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain BV21 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain JCR-44 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis partial 16S rRNA gene, isolate HL1RP1
Bacillus sp. ADMK36 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain MCCB 308 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain MCCB 319 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5572 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis partial 16S rRNA gene, isolate LK4HaP15
Bacillus pumilus strain KMDH10 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain ST15 16S ribosomal RNA gene, partial sequence
Bacillus altitudinis strain AA6-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-4 16S ribosomal RNA gene, partial sequence
Bacillus sp. NZ2-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. CRh14 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain CL21 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SBANHO9 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain C1AC3701 16S ribosomal RNA gene, partial sequence
Bacterium ARb28 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain BS37 16S ribosomal RNA gene, partial sequence
Azospirillum lipoferum partial 16S rRNA gene, isolate Azosp MdV 2
firmicutes | 15 leaves
Bacillus pumilus strain mv49b 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK74 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK22 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain JCR-65 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain DB3 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain AA5-5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 335-18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-12 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-5 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain WD204 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain RAS2-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. CL13 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SBG4 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain CM3701 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain OU93 16S ribosomal RNA gene, partial sequence
Bacillus safensis strain IHBB 11005 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain SBB12 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain B1 16S ribosomal RNA gene, partial sequence
Bacillus sp. MD-C14 16S ribosomal RNA gene, partial sequence
Bacillus pumilus strain HN-10 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5134 16S ribosomal RNA gene, partial sequence
Bacillus sp. RKAT-16 partial 16S rRNA gene, isolate RKAT-16
Endophytic bacterium SV715 16S ribosomal RNA gene, partial sequence
firmicutes | 9 leaves
Bacillus pumilus strain m350 16S ribosomal RNA gene, partial sequence
0.0003
0.0003

Bacillus licheniformis KT200463.1

Bacillus licheniformis strain KP062r 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT200463.1| **Length:** 1201 **Number of Matches:** 1

Range 1: 68 to 1014 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1700 bits(1884)	0.0	945/947(99%)	0/947(0%)	Plus/Plus

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Query  1     CGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGATTACTAGCG  60
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Sbjct  68    CGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCATGCTGATCCGCGATTACTAGCG  127

Query  61    ATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACTGAGAACAGATTTGTGGG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128   ATTCCAGCTTCACGCAGTCGAGTTGCAGACTGCGATCCGAACTGAGAACAGATTTGTGGG  187

Query  121   ATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTTCTGCCCATTGTAGCACGTGTGTAGC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188   ATTGGCTTAGCCTCGCGGCTTCGCTGCCCTTTGTTCTGCCCATTGTAGCACGTGTGTAGC  247

Query  181   CCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCG  307

Query  241   GCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGATCAAGGGTTGCGCTCGTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GCAGTCACCTTAGAGTGCCCAACTGAATGCTGGCAACTAAGATCAAGGGTTGCGCTCGTT  367

Query  301   GCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCAC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   GCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCAC  427

Query  361   TCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTTGTCAGAGGATGTCAAGACCTGGTAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TCTGCCCCCGAAGGGGAAGCCCTATCTCTAGGGTTGTCAGAGGATGTCAAGACCTGGTAA  487

Query  421   GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCA  547

Query  481   ATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  548   ATTCCTTTGAGTTTCAGTCTTGCGACCGTACTCCCCAGGCGGAGTGCTTAATGCGTTTGC  607

Query  541   TGCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCATCGTTTACGGCGTGGACT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCACTCATCGTTTACGGCGTGGACT  667

Query  601   ACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCGCCTCAGCGTCAGTTACAGAC  660
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Sbjct  668   ACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCGCCTCAGCGTCAGTTACAGAC  727

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Sbjct  728   CAGAGAGTCGCCTTCGCCACTGGTGTTCCTCCACATCTCTACGCATTTCACCGCTACACG  787

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Sbjct  908   ATTCCGGACAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAATTAGCCGTG  967

Query  901   GCTTTCTGGTTAGGTACCGTCAAGGTACCGCCCTATTCCAACGGGAC  947
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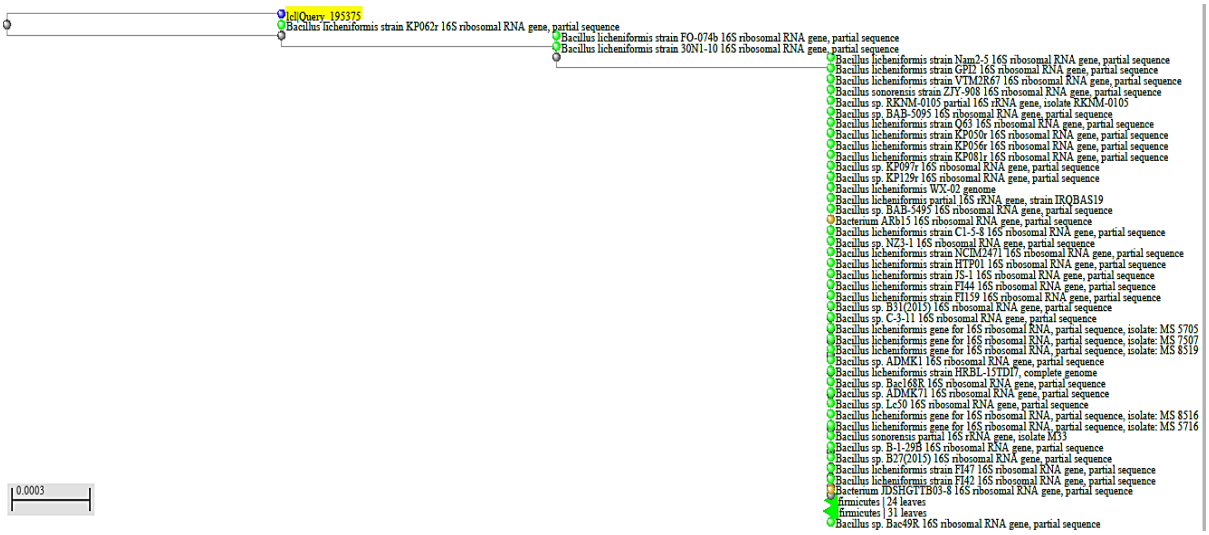
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Bacillus licheniformis strain FO-074b 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain 30N1-10 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Nam2-5 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain GPI2 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain VTM2R67 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain ZJY-908 16S ribosomal RNA gene, partial sequence
Bacillus sp. RKNM-0105 partial 16S rRNA gene, isolate RKNM-0105
Bacillus sp. BAB-5095 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Q63 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP050r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP056r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP081r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP097r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP129r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis WX-02 genome
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS19
Bacillus sp. BAB-5495 16S ribosomal RNA gene, partial sequence
Bacterium ARb15 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain C1-5-8 16S ribosomal RNA gene, partial sequence
Bacillus sp. NZ3-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NCIM2471 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain HTP01 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain JS-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI44 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI159 16S ribosomal RNA gene, partial sequence
Bacillus sp. B31(2015) 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-3-11 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 5705
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 7507
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 8519
Bacillus sp. ADMK1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain HRBL-15TDI7, complete genome
Bacillus sp. Bac168R 16S ribosomal RNA gene, partial sequence
Bacillus sp. ADMK71 16S ribosomal RNA gene, partial sequence
Bacillus sp. Lc50 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 8516
Bacillus licheniformis gene for 16S ribosomal RNA, partial sequence, isolate: MS 5716
Bacillus sonorensis partial 16S rRNA gene, isolate M33
Bacillus sp. B-1-29B 16S ribosomal RNA gene, partial sequence
Bacillus sp. B27(2015) 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI47 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI42 16S ribosomal RNA gene, partial sequence
Bacterium JDSHGTTB03-8 16S ribosomal RNA gene, partial sequence
firmicutes | 24 leaves
firmicutes | 31 leaves
Bacillus sp. Bac49R 16S ribosomal RNA gene, partial sequence
0.0003

9- The phylogenetic analysis of bacteria isolated from upper surfaces of water taps samples

Staphylococcus epidermidis KT887972.1

Staphylococcus epidermidis strain LIPOA/UEL_42 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT887972.1| **Length:** 1327 **Number of Matches:** 1

Range 1: 3 to 1051 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
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Sbjct  63    GGGATAACTTCGGGAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAAT  122

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Sbjct  123   AGTGAAAGACGGTTTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTA  182

Query  181   AGGTAACGGCTTACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACT  240
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Sbjct  363   GTTATTAGGGAAGAACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGA  422

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Sbjct  423   AAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCG  482

Query  481   GAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGG  540
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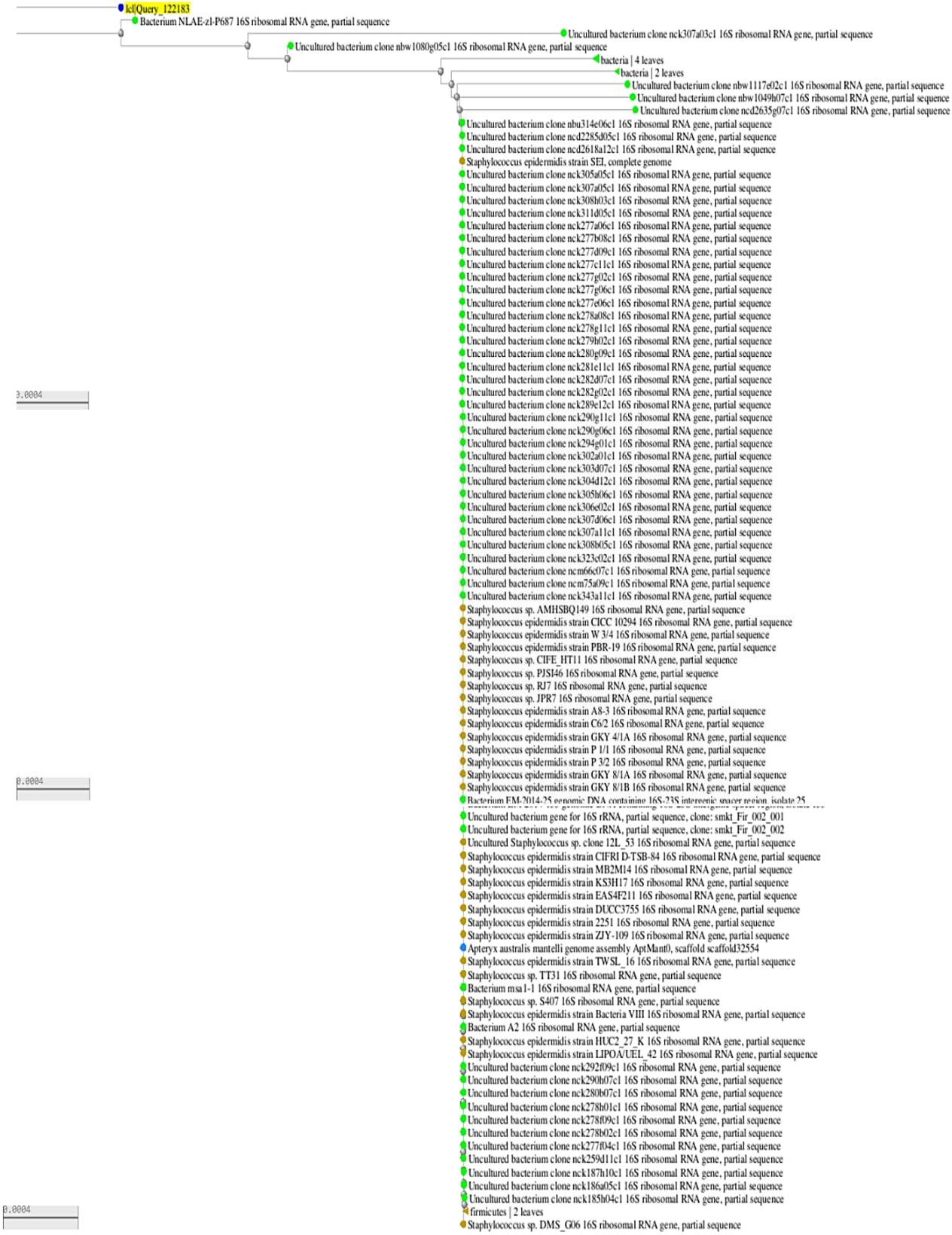
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Uncultured bacterium clone nbw1080g05c1 16S ribosomal RNA gene, partial sequence
bacteria | 4 leaves
bacteria | 2 leaves
Uncultured bacterium clone nbw1117e02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw1049h07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2635g07c1 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone ncd2618a12c1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain SEI, complete genome
Uncultured bacterium clone nck305a05c1 16S ribosomal RNA gene, partial sequence
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Staphylococcus sp. AMHSBQ149 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain CICC 10294 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain W 3/4 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain PBR-19 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. CIFE_HT11 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. PJSI46 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. RJ7 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. JPR7 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain A8-3 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain C6/2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain GKY 4/1A 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain P 1/1 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain P 3/2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain GKY 8/1A 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain GKY 8/1B 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium gene for 16S rRNA, partial sequence, clone: smkt_Fir_002_002
Uncultured Staphylococcus sp. clone 12L_53 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain CIFRI D-TSB-84 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain MB2M14 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain KS3H17 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain EAS4F211 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain DUCC3755 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain 2251 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain ZJY-109 16S ribosomal RNA gene, partial sequence
Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold32554
Staphylococcus epidermidis strain TWSL_16 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. TT31 16S ribosomal RNA gene, partial sequence
Bacterium msa1-1 16S ribosomal RNA gene, partial sequence
Staphylococcus sp. S407 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain Bacteria VIII 16S ribosomal RNA gene, partial sequence
Bacterium A2 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain HUC2_27_K 16S ribosomal RNA gene, partial sequence
Staphylococcus epidermidis strain LIPOA/UEL_42 16S ribosomal RNA gene, partial sequence
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firmicutes | 2 leaves
Staphylococcus sp. DMS_G06 16S ribosomal RNA gene, partial sequence
0.0004
0.0004
0.0004

Rothia amarae NR_029045.1

Rothia amarae strain J18 16S ribosomal RNA gene, partial sequence

Sequence ID: ref|NR_029045.1| **Length:** 1467 **Number of Matches:** 1

▶ See 1 more title(s)

Range 1: 98 to 1028 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1644 bits(1822)	0.0	924/931(99%)	1/931(0%)	Plus/Plus

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Query  61   GGTCTAATACCGGATATGACAAGGAACCGCATGGTTTTTTGTGGAAAGGGTTTGTACTGG  120
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Sbjct  158  GGTCTAATACCGGATATGACAAGGAACCGCATGGTTTTTTGTGGAAAGGGTTTGTACTGG  217

Query  121  TTTTAGATGGGCTCACGGCCTATCAGCTTGTTGGTGGGGTAATGGCTCACCAAGGCGACG  180
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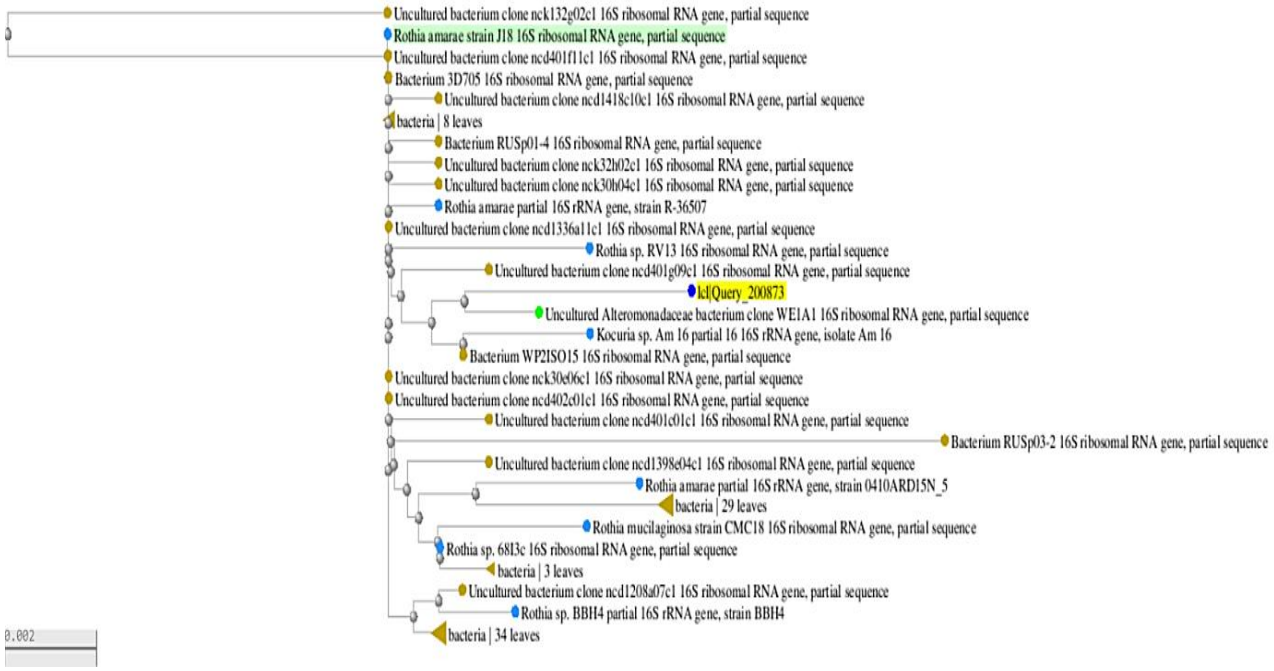
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Rothia amarae strain J18 16S ribosomal RNA gene, partial sequence
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Bacterium 3D705 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd1418c10c1 16S ribosomal RNA gene, partial sequence
bacteria | 8 leaves
Bacterium RUSp01-4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck32h02c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck30h04c1 16S ribosomal RNA gene, partial sequence
Rothia amarae partial 16S rRNA gene, strain R-36507
Uncultured bacterium clone ncd1336a11c1 16S ribosomal RNA gene, partial sequence
Rothia sp. RV13 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd401g09c1 16S ribosomal RNA gene, partial sequence
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Kocuria sp. Am 16 partial 16 16S rRNA gene, isolate Am 16
Bacterium WP2ISO15 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck30e06c1 16S ribosomal RNA gene, partial sequence
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Uncultured bacterium clone ncd401c01c1 16S ribosomal RNA gene, partial sequence
Bacterium RUSp03-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd1398e04c1 16S ribosomal RNA gene, partial sequence
Rothia amarae partial 16S rRNA gene, strain 0410ARD15N_5
bacteria | 29 leaves
Rothia mucilaginosa strain CMC18 16S ribosomal RNA gene, partial sequence
Rothia sp. 6813c 16S ribosomal RNA gene, partial sequence
bacteria | 3 leaves
Uncultured bacterium clone ncd1208a07c1 16S ribosomal RNA gene, partial sequence
Rothia sp. BBH4 partial 16S rRNA gene, strain BBH4
bacteria | 34 leaves
0.002

Delftia lacustris **KT958881.1**

Delftia lacustris strain BMCH-IB-C 142 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT958881.1| **Length:** 1360 **Number of Matches:** 1

Range 1: 355 to 1340 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1745 bits(1934)	0.0	980/986(99%)	3/986(0%)	Plus/Minus

```
Query  1     CCTACTTCTGGCGAGACCCGCTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1340  CCTACTTCTGGCGAGACCCGCTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAA  1281

Query  61    CGTATTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1280  CGTATTCACCGCGGCATGCTGATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAG  1221

Query  121   TTGCAGACTGCGATCCGGACTACGACTGGTTTTATGGGATTAGCTCCCCCTCGCGGGTTG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1220  TTGCAGACTGCGATCCGGACTACGACTGGTTTTATGGGATTAGCTCCCCCTCGCGGGTTG  1161

Query  181   GCAACCCTCTGTACCAGCCATTGTATGACGTGTGTAGCCCCACCTATAAGGGCCATGAGG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1160  GCAACCCTCTGTACCAGCCATTGTATGACGTGTGTAGCCCCACCTATAAGGGCCATGAGG  1101

Query  241   ACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCTCAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1100  ACTTGACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCTCAA  1041

Query  301   CTGAATGTAGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  CTGAATGTAGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA  981

Query  361   CGACACGAGCTGACGACAGCCATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAAT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   CGACACGAGCTGACGACAGCCATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAAT  921

Query  421   CCATCTCTGGAAACTTCCTGCCATGTCAAAGGTGGGTAAGGTTTTTCGCGTTGCATCGAA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   CCATCTCTGGAAACTTCCTGCCATGTCAAAGGTGGGTAAGGTTTTTCGCGTTGCATCGAA  861

Query  481   TTAAACCACATCATCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  860   TTAAACCACATCATCCACCGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTT  801

Query  541   GCGGCCGTACTCCCCAGGCGGTCAACTTCACGCGTTAGCTTCGTTACTGAGAAAACTAAT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   GCGGCCGTACTCCCCAGGCGGTCAACTTCACGCGTTAGCTTCGTTACTGAGAAAACTAAT  741

Query  601   TCCCAACAACCAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCCCAACAACCAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTG  681

Query  661   CTCCCCACGCTTTCGTGCATGAGCGTCAGTACAGGTCCAGGGGATTGCCTTCGCCATCGG  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   CTCCCCACGCTTTCGTGCATGAGCGTCAGTACAGGTCCAGGGGATTGCCTTCGCCATCGG  621

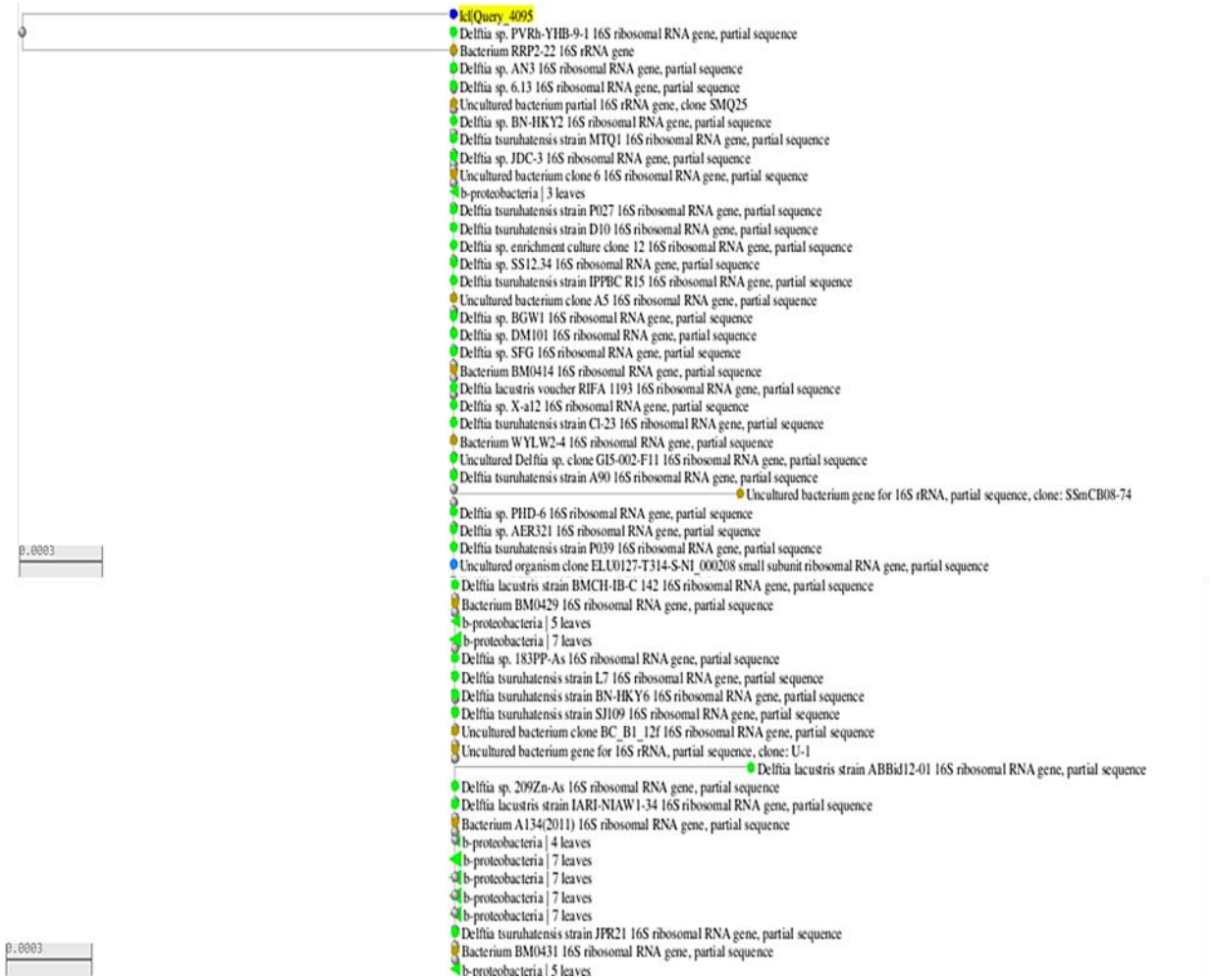
Query  721   TGTTCCTCCGCATATCTACGCATTTCACTGCTACACGCGGAATTCCATCCCCCTCTACCG  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   TGTTCCTCCGCATATCTACGCATTTCACTGCTACACGCGGAATTCCATCCCCCTCTACCG  561

Query  781   TACTCTAGCCATGCAGTCACAAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTG  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   TACTCTAGCCATGCAGTCACAAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTG  501

Query  841   TCTTACATAACCGCCTGCGCACGCTTTACGCCCAGTAATTCCGATTAACGCTCGCACCCT  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   TCTTACATAACCGCCTGCGCACGCTTTACGCCCAGTAATTCCGATTAACGCTCGCACCCT  441

Query  901   ACGTATTACCGCGGCTGCTGGCACGTAATTAGCCGGGGCTTATTCTTACGGTACCGTCAT  960
             |||||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Sbjct  440   ACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGTGCTTATTCTTACGGTACCGTCAT  381

Query  961   GGG-CCCCTGTATT--AAAGAGCTTT  983
             ||| |||||||||   || |||||||
Sbjct  380   GGGCCCCCTGTATTAGAAGGAGCTTT  355
```


kf|Query_4095
Delftia sp. PVRh-YHB-9-1 16S ribosomal RNA gene, partial sequence
Bacterium RRP2-22 16S rRNA gene
Delftia sp. AN3 16S ribosomal RNA gene, partial sequence
Delftia sp. 6.13 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone SMQ25
Delftia sp. BN-HKY2 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain MTQ1 16S ribosomal RNA gene, partial sequence
Delftia sp. JDC-3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 6 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 3 leaves
Delftia tsuruhatensis strain P027 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain D10 16S ribosomal RNA gene, partial sequence
Delftia sp. enrichment culture clone 12 16S ribosomal RNA gene, partial sequence
Delftia sp. SS12.34 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain IPPBC R15 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone A5 16S ribosomal RNA gene, partial sequence
Delftia sp. BGW1 16S ribosomal RNA gene, partial sequence
Delftia sp. DM101 16S ribosomal RNA gene, partial sequence
Delftia sp. SFG 16S ribosomal RNA gene, partial sequence
Bacterium BM0414 16S ribosomal RNA gene, partial sequence
Delftia lacustris voucher RIFA 1193 16S ribosomal RNA gene, partial sequence
Delftia sp. X-a12 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain CI-23 16S ribosomal RNA gene, partial sequence
Bacterium WYLW2-4 16S ribosomal RNA gene, partial sequence
Uncultured Delftia sp. clone GI5-002-F11 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain A90 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: SSmCB08-74
Delftia sp. PHD-6 16S ribosomal RNA gene, partial sequence
Delftia sp. AER321 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain P039 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0127-T314-S-NI_000208 small subunit ribosomal RNA gene, partial sequence
Delftia lacustris strain BMCH-IB-C 142 16S ribosomal RNA gene, partial sequence
Bacterium BM0429 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 5 leaves
b-proteobacteria | 7 leaves
Delftia sp. 183PP-As 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain L7 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain BN-HKY6 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain SJ109 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone BC_B1_12f 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: U-1
Delftia lacustris strain ABBid12-01 16S ribosomal RNA gene, partial sequence
Delftia sp. 209Zn-As 16S ribosomal RNA gene, partial sequence
Delftia lacustris strain IARI-NIAW1-34 16S ribosomal RNA gene, partial sequence
Bacterium A134(2011) 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 4 leaves
b-proteobacteria | 7 leaves
b-proteobacteria | 7 leaves
b-proteobacteria | 7 leaves
b-proteobacteria | 7 leaves
Delftia tsuruhatensis strain JPR21 16S ribosomal RNA gene, partial sequence
Bacterium BM0431 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 5 leaves
0.0003
0.0003

Pseudomonas aeruginosa KF680991.1

Pseudomonas aeruginosa strain ATHA23 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF680991.1| **Length:** 1115 **Number of Matches:** 1

Range 1: 98 to 1040 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1649 bits(1828)	0.0	933/943(99%)	2/943(0%)	Plus/Minus

```
Query  1     GTGATTGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGACATTCTGATTCACGAT  60
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  GTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGACATTCTGATTCACGAT  981

Query  61    TACTAGCGATTCCGACTTCACGCAGTCGAGTTGCAGACTGCGATCCGGACTACGATCGGT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   TACTAGCGATTCCGACTTCACGCAGTCGAGTTGCAGACTGCGATCCGGACTACGATCGGT  921

Query  121   TTTATGGGATTAGCTCCACCTCGCGGCTTGGCAACCCTTTGTACCGACCATTGTAGCACG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   TTTATGGGATTAGCTCCACCTCGCGGCTTGGCAACCCTTTGTACCGACCATTGTAGCACG  861

Query  181   TGTGTAGCCCTGGCCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  860   TGTGTAGCCCTGGCCGTAAGGGCCATGATGACTTGACGTCATCCCCACCTTCCTCCGGTT  801

Query  241   TGTCACCGGCAGTCTCCTTAGAGTGCCCACCCGAGGTGCTGGTAACTAAGGACAAGGGTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   TGTCACCGGCAGTCTCCTTAGAGTGCCCACCCGAGGTGCTGGTAACTAAGGACAAGGGTT  741

Query  301   GCGCTCGTTACGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   GCGCTCGTTACGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGC  681

Query  361   ACCTGTGTCTGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCAGCATGTCAAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTGTGTCTGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCAGCATGTCAAG  621

Query  421   GCCAGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   GCCAGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGG  561

Query  481   CCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTACTCCCCAGGCGGTCGACTTAT  501

Query  541   CGCGTTAGCTGCGCCACTAAGATCTCAAGGATCCCAACGGCTAGTCGACATCGTTTACGG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   CGCGTTAGCTGCGCCACTAAGATCTCAAGGATCCCAACGGCTAGTCGACATCGTTTACGG  441

Query  601   CGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTCAGTGTCAG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   CGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCACCTCAGTGTCAG  381

Query  661   TATCAGTCCAGGTGGTCGCCTTCGCCACTGGTGTTCCTTCCTATATCTACGCATTTCACC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   TATCAGTCCAGGTGGTCGCCTTCGCCACTGGTGTTCCTTCCTATATCTACGCATTTCACC  321

Query  721   GCTACACAGGAAATTCCACCACCCTCTACCGTACTCTAGCTCAGTAGTTTTGGATGCAAT  780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  320   GCTACACAGGAAATTCCACCACCCTCTACCGTACTCTAGCTCAGTAGTTTTGGATGCAGT  261

Query  781   TCCCAGGTTGAGCCCGGGGATTTCACATCCAACTTGCTGAACCACCTACGCGCGCTTTAC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   TCCCAGGTTGAGCCCGGGGATTTCACATCCAACTTGCTGAACCACCTACGCGCGCTTTAC  201

Query  841   GCCCAGTAATTCCGATTAACCCTTGCACCCTTCGTATTACCGCGGCTGCTGGCCCGAAGT  900
             |||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Sbjct  200   GCCCAGTAATTCCGATTAACGCTTGCACCCTTCGTATTACCGCGGCTGCTGGCACGAAGT  141

Query  901   TACCCGG-GCTTATTCTGTTGG-AACGTCAAAAAGCAAGGGAT  941
             || |||| |||||||||||||| ||||||||| ||||||| ||
Sbjct  140   TAGCCGGTGCTTATTCTGTTGGTAACGTCAAACAGCAAGGTAT  98
```


kl|Query_249999
Pseudomonas sp. H.A.K ton 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. DPs-19 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Pseudomonas aeruginosa strain Carb01 63, complete genome
Pseudomonas aeruginosa DK1 genome assembly Pseudomonas aeruginosa DK1 substr. NH57388A, chromosome : 1
Pseudomonas aeruginosa strain TH4 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA107 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA110 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA116 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA129 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA132 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA134 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA136 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA137 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA139 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA140 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA141 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA143 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA144 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA145 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA146 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA160 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA165 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NA168 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. RAU 305 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Ps15 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Ps8 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Ps6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ANF2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PS35 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa gene for 16S ribosomal RNA, partial sequence, strain: PD29
Pseudomonas aeruginosa gene for 16S ribosomal RNA, partial sequence, strain: BSS01
Pseudomonas aeruginosa strain PKS 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DASE-WM1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa partial 16S rRNA gene, isolate SHH
Pseudomonas aeruginosa partial 16S rRNA gene, isolate SHO
Bacterium YY3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZM130 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain S7PS5 16S ribosomal RNA gene, partial sequence
Staphylococcus sciuri strain SBANHCa14 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DSM 50071 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I2_6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I2_2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain GS-33 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain GS-31 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBL4 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain HBUZL-6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBL10 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBL8 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBL7 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBLDSB 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain JBLC 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PS3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 2-4-b-5 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 2-4-b-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 1-3-b-2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 1-4-b-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 1-5-b-2-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 1-4-b-9 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 3-5-b-5 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 3-4-b-2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 3-4-b-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 3-3-b-2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Z158 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. VIH2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-486 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-543 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-833 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-522 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-428 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-959 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ZJY-226 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain RRLP1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain SM-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Sp-A 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain EBL8 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain EBL6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain EBL5 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain LOCK 0999 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain LOCK 0998 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BjF3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain KRP1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. BAB-5039 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain duan1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BAL13 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain S04 90 genome
Bacterium WU1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ATHA23 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ATAI19 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BM6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain C37 16S ribosomal RNA gene, partial sequence
Pseudomonas otitidis strain FTYM11 16S ribosomal RNA gene, partial sequence
Bacterium C37 16S ribosomal RNA, partial sequence
g-proteobacteria | 5 leaves
Pseudomonas aeruginosa strain VV01 16S ribosomal RNA gene, partial sequence
0.0002

Delftia acidovorans (comamonas acid) **JX090199.1**

Delftia acidovorans strain AaI-4 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|JX090199.1| **Length:** 1412 **Number of Matches:** 1

Range 1: 399 to 1347 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1692 bits(1876)	0.0	945/949(99%)	1/949(0%)	Plus/Minus

```
Query  1     TCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGGCATGCTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  TCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGGCATGCTG  1288

Query  61    ATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAGTTGCAGACTGCGATCCGGACT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1287  ATCCGCGATTACTAGCGATTCCGACTTCACGCAGTCGAGTTGCAGACTGCGATCCGGACT  1228

Query  121   ACGACTGGTTTTATGGGATTAGCTCCCCCTCGCGGGTTGGCAACCCTCTGTACCAGCCAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  ACGACTGGTTTTATGGGATTAGCTCCCCCTCGCGGGTTGGCAACCCTCTGTACCAGCCAT  1168

Query  181   TGTATGACGTGTGTAGCCCCACCTATAAGGGCCATGAGGACTTGACGTCATCCCCACCTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TGTATGACGTGTGTAGCCCCACCTATAAGGGCCATGAGGACTTGACGTCATCCCCACCTT  1108

Query  241   CCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCAACTAAATGTAGCAACTAATGAC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107  CCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCAACTAAATGTAGCAACTAATGAC  1048

Query  301   AAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047  AAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCC  988

Query  361   ATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAATCCATCTCTGGAAACTTCCTGC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987   ATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAATCCATCTCTGGAAACTTCCTGC  928

Query  421   CATGTCAAAGGTGGGTAAGGTTTTTCGCGTTGCATCGAATTAAACCACATCATCCACCGC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927   CATGTCAAAGGTGGGTAAGGTTTTTCGCGTTGCATCGAATTAAACCACATCATCCACCGC  868

Query  481   TTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGCCGTACTCCCCAGGCGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  867   TTGTGCGGGTCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGCCGTACTCCCCAGGCGG  808

Query  541   TCAACTTCACGCGTTAGCTTCGTTACTGAGAAAACTAATTCCCAACAACCAGTTGACATC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  807   TCAACTTCACGCGTTAGCTTCGTTACTGAGAAAACTAATTCCCAACAACCAGTTGACATC  748

Query  601   GTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGTGCATG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   GTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGTGCATG  688

Query  661   AGCGTCAGTACAGGTCCAGGGGATTGCCTTCGCCATCGGTGTTCCTCCGCATATCTACGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687   AGCGTCAGTACAGGTCCAGGGGATTGCCTTCGCCATCGGTGTTCCTCCGCATATCTACGC  628

Query  721   ATTTCACTGCTACACGCGGAATTCCATCCCCCTCTACCGTACTCTAGCCATGCAGTCACA  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  627   ATTTCACTGCTACACGCGGAATTCCATCCCCCTCTACCGTACTCTAGCCATGCAGTCACA  568

Query  781   AATGCAGTTCCCA-GTTGAGCCCGGGGATTTCACATCTGTCTTACATAACCGCCTGCGCA  839
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
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lcl|Query_108535
Delftia acidovorans strain AaI-4 16S ribosomal RNA gene, partial sequence
Comamonas sp. 16S rRNA gene, isolate 158
Uncultured bacterium clone rRNA334 16S ribosomal RNA gene, partial sequence
Uncultured Delftia sp. clone EMP_K41 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp116-5a09.p1k 16S ribosomal RNA gene, partial sequence
Uncultured Delftia sp. clone IODP_305_1309D_water_sample_1200mbsf_2 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000061 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0181-T360-S-NIPCRAMgANa_000424 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000300 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000554 small subunit ribosomal RNA gene, partial sequence
Delftia sp. PP4_S2 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_33 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_185 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain A-B13B 16S ribosomal RNA gene, partial sequence
Delftia sp. BFE58M 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx11-1-075
Delftia sp. SR27 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_115 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S7 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000657 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000415 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000286 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000129 small subunit ribosomal RNA gene, partial sequence
Delftia lacustris strain 6S 16S ribosomal RNA gene, partial sequence
Delftia sp. R-41383 partial 16S rRNA gene, strain R-41383
Uncultured bacterium clone 16slp99-2e12.p1k 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 2 leaves
Delftia acidovorans strain B201 16S ribosomal RNA gene, partial sequence
Delftia sp. hg-1 16S ribosomal RNA gene, partial sequence
0.0008
Bacterium KR 1996/1_116 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S6 16S ribosomal RNA gene, partial sequence
Delftia sp. BFE58M 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx11-1-075
Delftia sp. SR27 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_115 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S7 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000657 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000415 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000286 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000129 small subunit ribosomal RNA gene, partial sequence
Delftia lacustris strain 6S 16S ribosomal RNA gene, partial sequence
Delftia sp. R-41383 partial 16S rRNA gene, strain R-41383
Uncultured bacterium clone 16slp99-2e12.p1k 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 2 leaves
Delftia acidovorans strain B201 16S ribosomal RNA gene, partial sequence
Delftia sp. hg-1 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_116 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S6 16S ribosomal RNA gene, partial sequence
Uncultured beta proteobacterium clone Alchichica_AL67_2_1B_104 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000365 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000473 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0024-T375-S-NIPCRAMgANb_000253 small subunit ribosomal RNA gene, partial sequence
Alcaligenes faecalis strain 18A 16S ribosomal RNA gene, partial sequence
bacteria | 4 leaves
Delftia sp. KAR43 16S ribosomal RNA gene, complete sequence
Delftia tsuruhatensis strain X15 16S ribosomal RNA gene, partial sequence
Delftia sp. 8-10 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_85 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S3 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000557 small subunit ribosomal RNA gene, partial sequence
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Uncultured organism clone ELU0182-T110-S-NIPCRAMgANa_000110 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000080 small subunit ribosomal RNA gene, partial sequence
Delftia acidovorans strain FGQ5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-2b06.w2k 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 4 leaves
Delftia sp. BFE41B 16S ribosomal RNA gene, partial sequence
Delftia sp. B0.09-91 16S ribosomal RNA gene, complete sequence
Bacterium KR 1979/21_152 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone AcL_G06
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000363 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000116 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000462 small subunit ribosomal RNA gene, partial sequence
Delftia acidovorans strain WR42 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp96-1a04.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp108-1f06.p1k 16S ribosomal RNA gene, partial sequence
Delftia acidovorans partial 16S rRNA gene, isolate NAT
Bacterium KR 1979/21_26 16S ribosomal RNA gene, partial sequence
Delftia acidovorans 16S ribosomal RNA gene, partial sequence
Delftia sp. BFE44L 16S ribosomal RNA gene, partial sequence
Delftia lacustris strain RK7 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_37 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S4 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S1 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000335 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000231 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000117 small subunit ribosomal RNA gene, partial sequence
Delftia acidovorans strain NBRC 14950 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-1b01.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp116-1e05.p1k 16S ribosomal RNA gene, partial sequence
Bacterium SV70AB2-3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx10-1-076
Delftia acidovorans strain S-B7A 16S ribosomal RNA gene, partial sequence
Bacterium KR 1979/21_108 16S ribosomal RNA gene, partial sequence
Delftia sp. S17 partial 16S rRNA gene, strain S17
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000645 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000507 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0028-T175-S-NIPCRAMgANa_000421 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000334 small subunit ribosomal RNA gene, partial sequence
Delftia acidovorans strain FGQ5 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain CL-9.07 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp97-1a10.p1k 16S ribosomal RNA gene, partial sequence
Delftia sp. P-101 partial 16S rRNA gene, strain P-101
Bacterium C0181 16S ribosomal RNA gene, partial sequence

Arthrobacter sanguinis NR_044399.1

Arthrobacter sanguinis strain 741 16S ribosomal RNA gene, partial sequence

Sequence ID: ref|NR_044399.1| **Length:** 1452 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 419 to 1390 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1727 bits(1914)	0.0	967/972(99%)	1/972(0%)	Plus/Minus

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Sbjct  1390  CGGGTGTTACCAACTTTCGTGACTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTC  1331

Query  61    ACCGCAGCGTTGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAG  120
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Sbjct  1330  ACCGCAGCGTTGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAG  1271

Query  121   ACCCCAATCCGAACTGAGACCGACTTTTTGGGATTAGCTCCACCTCACAGTATCGCAACC  180
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Sbjct  1270  ACCCCAATCCGAACTGAGACCGACTTTTTGGGATTAGCTCCACCTCACAGTATCGCAACC  1211

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Sbjct  1210  CTTTGTATCGGCCATTGTAGCATGCTTGAAGCCCAAGACATAAGGGGCATGATGATTTGA  1151

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Sbjct  1090  GTGCTGGCAACATAGAACGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGA  1031

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Sbjct  970   TGCGGCGGTCCGGTTCATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCATCGAATTAATC  911

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Query  721   TCTTCCTGATATCTGCGCATTCCACCGCTACACCAGGAATTCCAGTTACCCCTACATCAC  780
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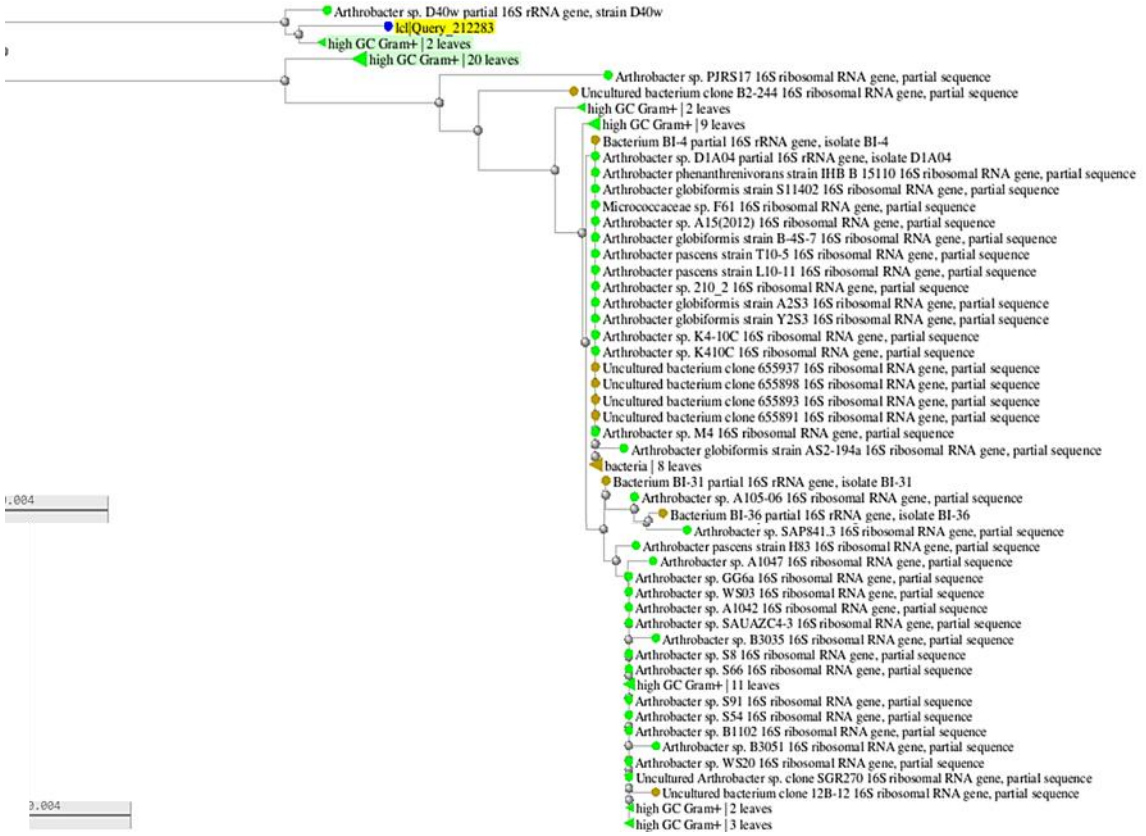
Arthrobacter sp. D40w partial 16S rRNA gene, strain D40w
lcl|Query_212283
high GC Gram+ | 2 leaves
high GC Gram+ | 20 leaves
Arthrobacter sp. PJRS17 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B2-244 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
high GC Gram+ | 9 leaves
Bacterium BI-4 partial 16S rRNA gene, isolate BI-4
Arthrobacter sp. D1A04 partial 16S rRNA gene, isolate D1A04
Arthrobacter phenanthrenivorans strain IHB B 15110 16S ribosomal RNA gene, partial sequence
Arthrobacter globiformis strain S11402 16S ribosomal RNA gene, partial sequence
Micrococcaceae sp. F61 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. A15(2012) 16S ribosomal RNA gene, partial sequence
Arthrobacter globiformis strain B-4S-7 16S ribosomal RNA gene, partial sequence
Arthrobacter pascens strain T10-5 16S ribosomal RNA gene, partial sequence
Arthrobacter pascens strain L10-11 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. 210_2 16S ribosomal RNA gene, partial sequence
Arthrobacter globiformis strain A2S3 16S ribosomal RNA gene, partial sequence
Arthrobacter globiformis strain Y2S3 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. K4-10C 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. K410C 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 655937 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 655898 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 655893 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 655891 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. M4 16S ribosomal RNA gene, partial sequence
Arthrobacter globiformis strain AS2-194a 16S ribosomal RNA gene, partial sequence
bacteria | 8 leaves
Bacterium BI-31 partial 16S rRNA gene, isolate BI-31
Arthrobacter sp. A105-06 16S ribosomal RNA gene, partial sequence
Bacterium BI-36 partial 16S rRNA gene, isolate BI-36
Arthrobacter sp. SAP841.3 16S ribosomal RNA gene, partial sequence
Arthrobacter pascens strain H83 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. A1047 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. GG6a 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. WS03 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. A1042 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. SAUAZC4-3 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. B3035 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. S8 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. S66 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 11 leaves
Arthrobacter sp. S91 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. S54 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. B1102 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. B3051 16S ribosomal RNA gene, partial sequence
Arthrobacter sp. WS20 16S ribosomal RNA gene, partial sequence
Uncultured Arthrobacter sp. clone SGR270 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 12B-12 16S ribosomal RNA gene, partial sequence
high GC Gram+ | 2 leaves
high GC Gram+ | 3 leaves

Delftia acidovorans (comamonas acid) **KJ781879.1**

Delftia acidovorans strain B208 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ781879.1| **Length:** 1421 **Number of Matches:** 1

Range 1: 428 to 1376 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1599 bits(1772)	0.0	927/950(98%)	3/950(0%)	Plus/Minus

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Sbjct  1376  GGCGAGACCCGCTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCAC  1317

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Sbjct  1136  CATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCAACTAAATGTA  1077

Query  301   GCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAG  360
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Sbjct  1076  GCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAG  1017

Query  361   CTGACGACAGCCATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAATCCATCTCTG  420
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Sbjct  1016  CTGACGACAGCCATGCAGCACCTGTGTGCAGGTTCTCTTTCGAGCACGAATCCATCTCTG  957

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Query  601   CCAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG  660
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Sbjct  776   CCAGTTGACATCGTTTAGGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACG  717

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Sbjct  716   CTTTCGTGCATGAGCGTCAGTACAGGTCCAGGGGATTGCCTTCGCCATCGGTGTTCCTCC  657

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Query  841   ACCCCCTGGGCACGCTTTACCCCCAAAAATTCC-AATAAAGCTTGCCCCCTACGTATTAC  899
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Query  900   CCCGGCTGGTGGGGCCGTATTTAACCGG-GGTTATTCTTACGGAACCGTC  948
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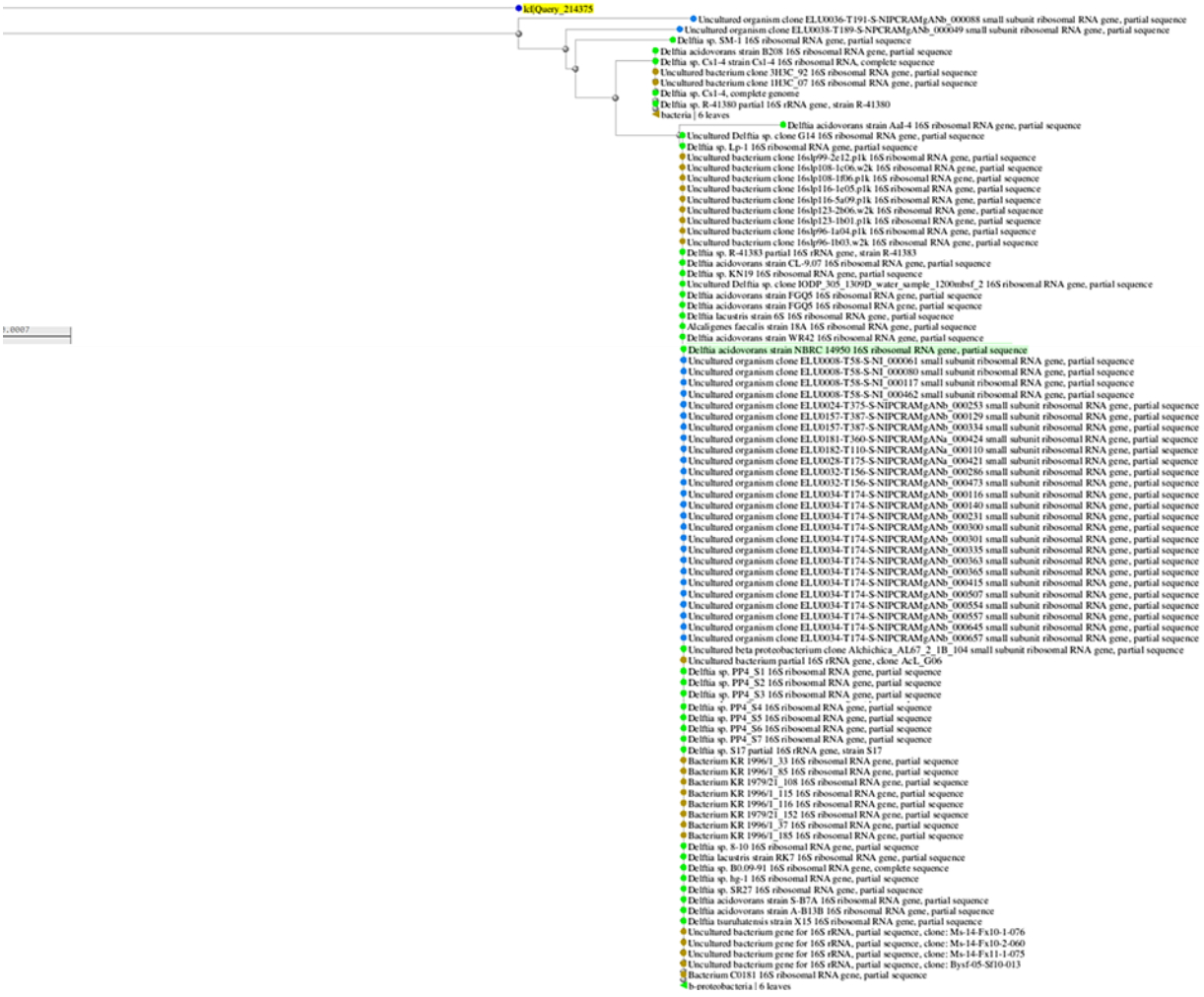
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Uncultured organism clone ELU0038-T189-S-NPCRAMgANb_000049 small subunit ribosomal RNA gene, partial sequence
Delftia sp. SM-1 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain B208 16S ribosomal RNA gene, partial sequence
Delftia sp. Cs1-4 strain Cs1-4 16S ribosomal RNA, complete sequence
Uncultured bacterium clone 1H3C_92 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 1H3C_07 16S ribosomal RNA gene, partial sequence
Delftia sp. Cs1-4, complete genome
Delftia sp. R-41380 partial 16S rRNA gene, strain R-41380
bacteria | 6 leaves
Delftia acidovorans strain Aal-4 16S ribosomal RNA gene, partial sequence
Uncultured Delftia sp. clone G14 16S ribosomal RNA gene, partial sequence
Delftia sp. Lp-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp99-2e12.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp108-1c06.w2k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp108-1f06.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp116-1e05.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp116-5a09.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-2b06.w2k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp123-1b01.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp96-1a04.p1k 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp96-1b03.w2k 16S ribosomal RNA gene, partial sequence
Delftia sp. R-41383 partial 16S rRNA gene, strain R-41383
Delftia acidovorans strain CL-9.07 16S ribosomal RNA gene, partial sequence
Delftia sp. KN19 16S ribosomal RNA gene, partial sequence
Uncultured Delftia sp. clone IODP_305_1309D_water_sample_1200mbsf_2 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain FGQ5 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain FGQ5 16S ribosomal RNA gene, partial sequence
Delftia lacustris strain 6S 16S ribosomal RNA gene, partial sequence
Alcaligenes faecalis strain 18A 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain WR42 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain NBRC 14950 16S ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000061 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000080 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000117 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0008-T58-S-NI_000462 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0024-T375-S-NIPCRAMgANb_000253 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000129 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0157-T387-S-NIPCRAMgANb_000334 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0181-T360-S-NIPCRAMgANa_000424 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0182-T110-S-NIPCRAMgANa_000110 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0028-T175-S-NIPCRAMgANa_000421 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000286 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0032-T156-S-NIPCRAMgANb_000473 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000116 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000140 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000231 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000300 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000301 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000335 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000363 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000365 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000415 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000507 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000554 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000557 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000645 small subunit ribosomal RNA gene, partial sequence
Uncultured organism clone ELU0034-T174-S-NIPCRAMgANb_000657 small subunit ribosomal RNA gene, partial sequence
Uncultured beta proteobacterium clone Akhichica_AL67_2_1B_104 small subunit ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone AcL_G06
Delftia sp. PP4_S1 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S2 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S3 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S4 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S5 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S6 16S ribosomal RNA gene, partial sequence
Delftia sp. PP4_S7 16S ribosomal RNA gene, partial sequence
Delftia sp. S17 partial 16S rRNA gene, strain S17
Bacterium KR 1996/1_33 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_85 16S ribosomal RNA gene, partial sequence
Bacterium KR 1979/2I_108 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_115 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_116 16S ribosomal RNA gene, partial sequence
Bacterium KR 1979/2I_152 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_37 16S ribosomal RNA gene, partial sequence
Bacterium KR 1996/1_185 16S ribosomal RNA gene, partial sequence
Delftia sp. 8-10 16S ribosomal RNA gene, partial sequence
Delftia lacustris strain RK7 16S ribosomal RNA gene, partial sequence
Delftia sp. B0.09-91 16S ribosomal RNA gene, complete sequence
Delftia sp. hg-1 16S ribosomal RNA gene, partial sequence
Delftia sp. SR27 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain S-B7A 16S ribosomal RNA gene, partial sequence
Delftia acidovorans strain A-B13B 16S ribosomal RNA gene, partial sequence
Delftia tsuruhatensis strain X15 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx10-1-076
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx10-2-060
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Ms-14-Fx11-1-075
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: Bysf-05-Sf10-013
Bacterium C0181 16S ribosomal RNA gene, partial sequence
b-proteobacteria | 6 leaves

Bacillus cereus GQ344804.1

Bacillus cereus strain DC2 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|GQ344804.1| **Length:** 1424 **Number of Matches:** 1

Range 1: 442 to 1382 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1397 bits(1548)	0.0	883/941(94%)	11/941(1%)	Plus/Minus

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Query  1     CAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1382  CAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCA  1323

Query  61    TGCTGATCCGCGATTACTAGCGATTCCAACTTCATGTAGGCGAGTTGCAGCCGACAATCC  120
             |||||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct  1322  TGCTGATCCGCGATTACTAGCGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCC  1263

Query  121   GAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1262  GAACTGAGAACGGTTTTATGAGATTAGCTCCACCTCGCGGTCTTGCAGCTCTTTGTACCG  1203

Query  181   TCCATTGTATCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCC  240
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1202  TCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCC  1143

Query  241   ACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACT  300
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Sbjct  1142  ACCTTCCTCCGGTTTGTCACCGGCAGTCACCTTAGAGTGCCCAACTTAATGATGGCAACT  1083

Query  301   AGAATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGATCTGAAC  360
             |  |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1082  AAGATCAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACG  1023

Query  361   ACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGACAAACCCTATCTCTAGGGTTTTC  420
             |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Sbjct  1022  ACAACCATGCACCACCTGTCACTCTGCTCCCGAAGGAGAAGCCCTATCTCTAGGGTTTTC  963

Query  421   A-AGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCA  479
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  962   AGAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCA  903

Query  480   CCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAG  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  902   CCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAGCCTTGCGGCCGTACTCCCCAG  843

Query  540   GCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTATCA  599
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  842   GCGGAGTGCTTAATGCGTTAACTTCAGCACTAAAGGGCGGAAACCCTCTAACACTTAGCA  783

Query  600   CTCATCGTTTACGGCGTGGACTACCGGGATATCTAATCGTGTTTGCTCCCCACTCTTTCG  659
             |||||||||||||||||||||||| || ||||||||| ||||||||||||||| ||||||
Sbjct  782   CTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCG  723

Query  660   CGCCTCAGTGTCAATTACGGACCA-AAAGTCCCCTTCCCCACTGGTGTTCCTCCATATCT  718
             |||||||||||| |||| ||||| |||||| ||||| ||||||||||||||||||||||
Sbjct  722   CGCCTCAGTGTCAGTTACAGACCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCATATCT  663

Query  719   CTACCCTTTTCACCGCTACACATGAAATT-CACTTTCCTCTTCTGCACTCAAGTCTCCCA  777
             |||| | |||||||||||||||| |||| ||||||||||||||||||||||||||||||
Sbjct  662   CTACGCATTTCACCGCTACACATGGAATTCCACTTTCCTCTTCTGCACTCAAGTCTCCCA  603

Query  778   GTTTCCAATGACCC-CCACGGTTGACCCG-GGGTTTTCACTTCAAACTTAA-AAACC-CC  833
             |||||||||||||| |||||||||| ||| ||| |||||| ||| |||||| ||||| ||
Sbjct  602   GTTTCCAATGACCCTCCACGGTTGAGCCGTGGGCTTTCACATCAGACTTAAGAAACCACC  543

Query  834   GGCCCGCCCTTTAC-CCCAAT-ATTCCAAGAAACCCTTGCCCCCTACTTATTACC-Cggg  890
              || ||| |||||| |||||| |||||    ||| |||||| ||||| |||||||  |||
Sbjct  542   TGCGCGCGCTTTACGCCCAATAATTCCGGATAACGCTTGCCACCTACGTATTACCGCGGC  483

Query  891   gggggCCCGAATTTACCCGGGGTTTTTCTGG-TAGGAACC  930
               |  ||| || | ||| ||| || |||||||| |||| |||
Sbjct  482   TGCTGGCACGTAGTTAGCCGTGGCTTTTCTGGTTAGGTACC  442
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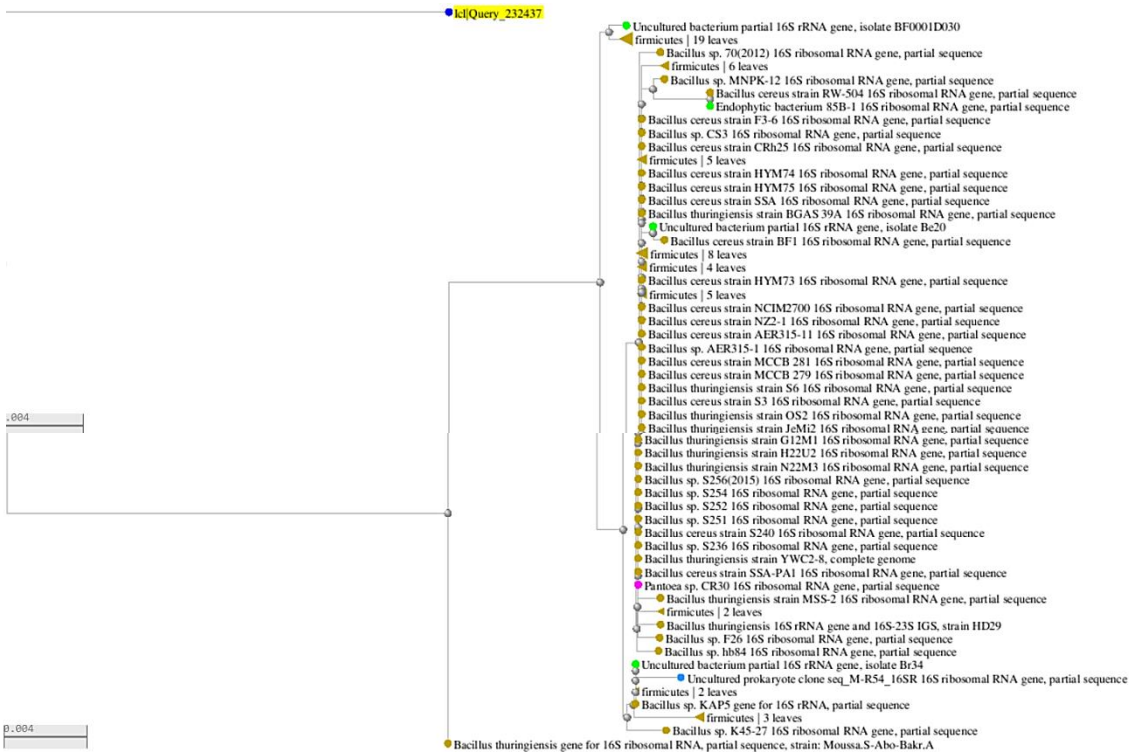
lcl|Query_232437
Uncultured bacterium partial 16S rRNA gene, isolate BF0001D030
firmicutes | 19 leaves
Bacillus sp. 70(2012) 16S ribosomal RNA gene, partial sequence
firmicutes | 6 leaves
Bacillus sp. MNPK-12 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain RW-504 16S ribosomal RNA gene, partial sequence
Endophytic bacterium 85B-1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain F3-6 16S ribosomal RNA gene, partial sequence
Bacillus sp. CS3 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain CRh25 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus cereus strain HYM74 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain HYM75 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain SSA 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain BGAS 39A 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Be20
Bacillus cereus strain BF1 16S ribosomal RNA gene, partial sequence
firmicutes | 8 leaves
firmicutes | 4 leaves
Bacillus cereus strain HYM73 16S ribosomal RNA gene, partial sequence
firmicutes | 5 leaves
Bacillus cereus strain NCIM2700 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain NZ2-1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain AER315-11 16S ribosomal RNA gene, partial sequence
Bacillus sp. AER315-1 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MCCB 281 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain MCCB 279 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain S6 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain S3 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain OS2 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain JeMi2 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain G12M1 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain H22U2 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain N22M3 16S ribosomal RNA gene, partial sequence
Bacillus sp. S256(2015) 16S ribosomal RNA gene, partial sequence
Bacillus sp. S254 16S ribosomal RNA gene, partial sequence
Bacillus sp. S252 16S ribosomal RNA gene, partial sequence
Bacillus sp. S251 16S ribosomal RNA gene, partial sequence
Bacillus cereus strain S240 16S ribosomal RNA gene, partial sequence
Bacillus sp. S236 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain YWC2-8, complete genome
Bacillus cereus strain SSA-PA1 16S ribosomal RNA gene, partial sequence
Pantoea sp. CR30 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis strain MSS-2 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus thuringiensis 16S rRNA gene and 16S-23S IGS, strain HD29
Bacillus sp. F26 16S ribosomal RNA gene, partial sequence
Bacillus sp. hb84 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate Br34
Uncultured prokaryote clone seq_M-R54_16SR 16S ribosomal RNA gene, partial sequence
firmicutes | 2 leaves
Bacillus sp. KAP5 gene for 16S rRNA, partial sequence
firmicutes | 3 leaves
Bacillus sp. K45-27 16S ribosomal RNA gene, partial sequence
Bacillus thuringiensis gene for 16S ribosomal RNA, partial sequence, strain: Moussa.S-Abo-Bakr.A
.004
0.004

10- The phylogenetic analysis of bacteria isolated from used toothbrushes samples

Roseomonas mucosa KF247232.1

Roseomonas mucosa strain SM14032013 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF247232.1| **Length:** 1455 **Number of Matches:** 1

Range 1: 102 to 983 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1572 bits(1742)	0.0	879/883(99%)	1/883(0%)	Plus/Plus

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Query  1    GGACGGGTGAGTAACGCGTAGGAACGTGTCCTGAGGTGGGGGACAACCCCGGGAAACTGG  60
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Sbjct  102  GGACGGGTGAGTAACGCGTAGGAACGTGTCCTGAGGTGGGGGACAACCCCGGGAAACTGG  161

Query  61   GGCTAATACCGCATATGGGCTGAGGCCCAAAGCCGAGAGGCGCCTTTGGAGCGGCCTGCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  162  GGCTAATACCGCATATGGGCTGAGGCCCAAAGCCGAGAGGCGCCTTTGGAGCGGCCTGCG  221

Query  121  TCCGATTAGGTAGTTGGTGGGGTAAAGGCCTACCAAGCCTGCGATCGGTAGCTGGTCTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  222  TCCGATTAGGTAGTTGGTGGGGTAAAGGCCTACCAAGCCTGCGATCGGTAGCTGGTCTGA  281

Query  181  GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  282  GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGT  341

Query  241  GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGGGTGAAGAAGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  342  GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGGGTGAAGAAGGT  401

Query  301  CTTCGGATCGTAAAGCCCTTTCGACGGGGACGATGATGACGGTACCCGTAGAAGAAGCCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  402  CTTCGGATCGTAAAGCCCTTTCGACGGGGACGATGATGACGGTACCCGTAGAAGAAGCCC  461

Query  361  CGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  462  CGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATTA  521

Query  421  CTGGGCGTAAAGGGCGCGTAGGCGGCGGCCCAAGTCAGGCGTGAAATTCCTGGGCTCAAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  522  CTGGGCGTAAAGGGCGCGTAGGCGGCGGCCCAAGTCAGGCGTGAAATTCCTGGGCTCAAC  581

Query  481  CTGGGGACTGCGCTTGATACTGGGTTGCTTGAGGATGGAAGAGGCTCGTGGAATTCCCAG  540
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Sbjct  582  CTGGGGACTGCGCTTGATACTGGGTTGCTTGAGGATGGAAGAGGCTCGTGGAATTCCCAG  641

Query  541  TGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCGAGCTGGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  642  TGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCGAGCTGGT  701

Query  601  CCATTACTGACGCTGAGGCGCGACAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  702  CCATTACTGACGCTGAGGCGCGACAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG  761

Query  661  TCCACGCCGTAAACGATGTGCGCTGGATGTTGGGGCCCATAGGGTCTCAGTGTCGTAGCC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  762  TCCACGCCGTAAACGATGTGCGCTGGATGTTGGGGCCCATAGGGTCTCAGTGTCGTAGCC  821

Query  721  AACGCGGTAAGCGCACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  822  AACGCGGTAAGCGCACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGA  881

Query  781  CGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAAAACCCTT  840
            |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Sbjct  882  CGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAA-CCTT  940

Query  841  ACCAGCCCTTGACATGGTCACGACCGGTCCAAAAATGGACTTT  883
            |||||||||||||||||||||||||||| | |||||||||
Sbjct  941  ACCAGCCCTTGACATGGTCACGACCGGTCCAGAGATGGACTTT  983
```


kl|Query_10625
Uncultured bacterium clone ncd2760c02c1 16S ribosomal RNA gene, partial sequence
Roseomonas mucosa strain MDA5527 16S ribosomal RNA gene, partial sequence
Candidatus Roseomonas massiliae 1461A 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd752e03c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 5 leaves
bacteria | 2 leaves
Uncultured bacterium clone ncd648f11c1 16S ribosomal RNA gene, partial sequence
Roseomonas sp. CB 286483 partial 16S rRNA gene, strain CB 286483
bacteria | 2 leaves
Roseomonas sp. CMS4Y-2-2 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 5 leaves
Roseomonas mucosa strain EHFS2_S05Hb 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd507e12c1 16S ribosomal RNA gene, partial sequence
bacteria | 5 leaves
bacteria | 2 leaves
Candidatus Roseomonas massiliae 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 5 leaves
Roseomonas terpenica partial 16S rRNA gene, type strain DT
Uncultured bacterium clone ncd510c02c1 16S ribosomal RNA gene, partial sequence
bacteria | 5 leaves
bacteria | 2 leaves
Roseomonas mucosa strain SM14032013 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 5 leaves
Roseomonas mucosa strain ES_21con 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd513a06c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Roseomonas sp. BZ44 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 34 leaves
0.0003

Stenotrophomonas maltophilia LN890169.1

Stenotrophomonas maltophilia partial 16S rRNA gene, strain M83

Sequence ID: emb|LN890169.1| **Length:** 1688 **Number of Matches:** 1

Range 1: 190 to 1127 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1665 bits(1846)	0.0	933/938(99%)	1/938(0%)	Plus/Plus

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Query  1     TGGGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTCTGTCGTGGGGGATA  60
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Sbjct  190   TGGGTGGCGAGTGGCGGACGGGTGAGGAATACATCGGAATCTACTCTGTCGTGGGGGATA  249

Query  61    ACGTAGGGAAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGATCTTCG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   ACGTAGGGAAACTTACGCTAATACCGCATACGACCTACGGGTGAAAGCAGGGGATCTTCG  309

Query  121   GACCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCCAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310   GACCTTGCGCGATTGAATGAGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCCAC  369

Query  181   CAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAACTGAGACACG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370   CAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAACTGAGACACG  429

Query  241   GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATC  300
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Sbjct  430   GTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATC  489

Query  301   CAGCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTTTGTTGGGAAAGA  360
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Sbjct  490   CAGCCATACCGCGTGGGTGAAGAAGGCCTTCGGGTTGTAAAGCCCTTTTGTTGGGAAAGA  549

Query  361   AATCCAGCTGGCTAATACCCGGTTGGGATGACGGTACCCAAAGAATAAGCACCGGCTAAC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550   AATCCAGCTGGCTAATACCCGGTTGGGATGACGGTACCCAAAGAATAAGCACCGGCTAAC  609

Query  421   TTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTACTCGGAATTACTGGGCGT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610   TTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTACTCGGAATTACTGGGCGT  669

Query  481   AAAGCGTGCGTAGGTGGTCGTTTAAGTCCGTTGTGAAAGCCCTGGGCTCAACCTGGGAAC  540
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Sbjct  670   AAAGCGTGCGTAGGTGGTCGTTTAAGTCCGTTGTGAAAGCCCTGGGCTCAACCTGGGAAC  729

Query  541   TGCAGTGGATACTGGGCGACTAGAGTGTGGTAGAGGGTAGCGGAATTCCTGGTGTAGCAG  600
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Sbjct  730   TGCAGTGGATACTGGGCGACTAGAGTGTGGTAGAGGGTAGCGGAATTCCTGGTGTAGCAG  789

Query  601   TGAAATGCGTAGAGATCAGGAGGAACATCCATGGCGAAGGCAGCTACCTGGACCAACACT  660
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Sbjct  790   TGAAATGCGTAGAGATCAGGAGGAACATCCATGGCGAAGGCAGCTACCTGGACCAACACT  849

Query  661   GACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  850   GACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC  909

Query  721   CTAAACGATGCGAACTGGATGTTGGGTGCAATTTGGCACGCAGTATCGAAGCTAACGCGT  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  910   CTAAACGATGCGAACTGGATGTTGGGTGCAATTTGGCACGCAGTATCGAAGCTAACGCGT  969

Query  781   TAAGTTCGCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTC-AAGGAATTGACGGGGGC  839
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  970   TAAGTTCGCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGC  1029

Query  840   CCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTGGCC  899
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1030  CCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGCC  1089

Query  900   TTGACATGTCGAGAACTTTCCAAAAATGGATGGGGGCC  937
             ||||||||||||||||||||| | ||||||||| |||
Sbjct  1090  TTGACATGTCGAGAACTTTCCAGAGATGGATGGGTGCC  1127
```


Stenotrophomonas maltophilia strain ST1 16S ribosomal RNA gene, partial sequence
kf|Query_149727
Uncultured bacterium partial 16S rRNA gene, clone Clone_57
Pseudomonas sp. LS3K gene for 16S ribosomal RNA, partial sequence
Bacterium INBio_40547 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 121 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 221 16S ribosomal RNA gene, partial sequence
Bacterium AM0277 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Gammaproteobacteria bacterium S3_AA2 16S ribosomal RNA gene, partial sequence
Bacterium AM0023 16S ribosomal RNA gene, partial sequence
Bacterium AM0015 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 14 leaves
Uncultured bacterium clone nbt78807 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw957h07c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd520712c1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3121 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3149 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 2A952 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-G-NA3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-S-PYD2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-LS-R2A6 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 2324 16S ribosomal RNA gene, partial sequence
Pseudomonas hibiscicola strain SH8 16S ribosomal RNA gene, partial sequence
Pseudomonas geniculata strain YJART-1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain HUC1_23a_K 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. CS18 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. pT2-440Y 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain IR88 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. ZW518 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. U1369-101122-SW177 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain A1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-LS-TSA5 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-J-MA2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-J-PYD4 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain JKR32b 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3155 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC2127 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC1012 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. VFI 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. OUC_Est10 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. TSG4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbt24d12 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia partial 16S rRNA gene, strain M83
Pseudomonas hibiscicola strain SD8 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain JN263 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain A2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PCA_D6_5 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-LS-PYD2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-J-PDA7 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd1000c08c1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain AlsB4 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC2128 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3052 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone A1H1M9 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Pseudomonas sp. 261(2015) 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain IR48 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain T-B7D 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. SAUBS3-3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 2364 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-S-PDA4 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-S-TSA3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-S-R2A2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 2A9N6 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3150 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3122 16S ribosomal RNA gene, partial sequence
Uncultured Stenotrophomonas sp. clone A6H6M9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. VI 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbt237h03 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Stenotrophomonas maltophilia strain IR97 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain CYJ 1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain LAMA 900 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain A3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-J-PDA4 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-J-PYD1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. C-S-PYD6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 3-42035 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC2160 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC3148 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain BAC2031 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd183f08c1 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
0.0003
0003

Pseudomonas aeruginosa KR815846.1

Pseudomonas aeruginosa strain Pse12 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KR815846.1| **Length:** 1444 **Number of Matches:** 1

Range 1: 34 to 999 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1685 bits(1868)	0.0	955/966(99%)	5/966(0%)	Plus/Plus

```
Query  1    TGGATTCNGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAAC  60
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34   TGGATTCAGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAAC  93

Query  61   GTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGATCTTCGGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  94   GTCCGGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGATCTTCGGA  153

Query  121  CCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  154  CCTCACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCA  213

Query  181  AGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  214  AGGCGACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGT  273

Query  241  CCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  274  CCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCA  333

Query  301  GCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  334  GCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAG  393

Query  361  GGCAGTAAGTTAATACCTTGCTGTTTTGACGTTACCAACAGAATAAGCACCGGCTAACTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  394  GGCAGTAAGTTAATACCTTGCTGTTTTGACGTTACCAACAGAATAAGCACCGGCTAACTT  453

Query  421  CGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  454  CGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAA  513

Query  481  AGCGCGCGTAGGTGGTTCAGCAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTG  540
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Sbjct  514  AGCGCGCGTAGGTGGTTCAGCAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTG  573

Query  541  CATCCAAAACTACTGAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTG  600
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Sbjct  574  CATCCAAAACTACTGAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTG  633

Query  601  AAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGA  660
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Sbjct  634  AAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGA  693

Query  661  CACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  694  CACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGT  753

Query  721  AAACGATGTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCGCAGCTAACGCGATAA  780
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Sbjct  754  AAACGATGTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCGCAGCTAACGCGATAA  813

Query  781  GTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCG  840
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Sbjct  814  GTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCG  873

Query  841  CACAAGCGGTGGAGCATGTGGTTTAATTCTAAGCAACGCGAAAAACCTTACCTGGGCCTT  900
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  874  CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAAAACCTTACCTGGGCCTT  933

Query  901  GACATGCTGAAAACTTTCCAAAAATGGATTGGGGCCTTC--GGAACTC-AAACCCAGG--  955
            |||||||||| |||||||||| ||||||||| |||||| |||||||| |||| ||||
Sbjct  934  GACATGCTGAGAACTTTCCAAAGATGGATTGGTGCCTTCCGGGAACTCAAAACACAGGGT  993

Query  956  GCTGCA  961
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Sbjct  994  GCTGCA  999
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lcl|Query_204185
Pseudomonas aeruginosa strain Pse12 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Q5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone 16sps16-2g11.p1k
Pseudomonas aeruginosa strain KAR21 16S ribosom
Pseudomonas aeruginosa DHS01, complete genome
Pseudomonas aeruginosa strain PT121 16S ribosom
Uncultured bacterium clone P3D1-622 16S ribosom
Uncultured bacterium clone P3D1-629 16S ribosom
Uncultured bacterium clone P3D5-491 16S ribosom
Uncultured bacterium clone P3D1-455 16S ribosom
Uncultured bacterium clone P3D1-406 16S ribosom
Uncultured bacterium clone P3D1-429 16S ribosom
Uncultured bacterium clone P3D1-420 16S ribosom
Uncultured bacterium clone P3D5-558 16S ribosom
Uncultured bacterium clone P3D1-392 16S ribosom
Uncultured bacterium clone P3D5-740 16S ribosom
Uncultured bacterium clone P3D5-513 16S ribosom
Uncultured bacterium clone P3D5-681 16S ribosom
Uncultured bacterium clone P3D5-568 16S ribosom
Uncultured bacterium clone P3D5-754 16S ribosom
Uncultured bacterium clone P3D5-742 16S ribosom
Uncultured bacterium clone P3D5-768 16S ribosom
Uncultured bacterium clone P3D5-514 16S ribosom
Uncultured bacterium clone P3D5-521 16S ribosom
Uncultured bacterium clone P3D5-723 16S ribosom
Uncultured bacterium clone P3D5-752 16S ribosom
Uncultured bacterium clone P3D5-515 16S ribosom
Uncultured bacterium clone P3D5-492 16S ribosom
Uncultured bacterium clone P3D5-729 16S ribosom
Uncultured bacterium clone P3D5-699 16S ribosom
Uncultured gamma proteobacterium clone FTL229
g-proteobacteria | 3 leaves
g-proteobacteria | 5 leaves
g-proteobacteria | 2 leaves
Pseudomonas aeruginosa strain 28 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-108 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-108-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R5-327 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R5-761 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-801 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R8-588 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 2 leaves
Pseudomonas aeruginosa strain PA007 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BN2 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. L10 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NBAII RFF-7 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R1-6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R1-6-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-106 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-107-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-109 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-106-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-110-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-107 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R3-117-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-336 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-336-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-360 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-360-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R2-110 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-756 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-757 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-789 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R5-425 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-363 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-401 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-401-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-421 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-765 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-520 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-520-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-549 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-580 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R4-423 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-583 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R7-766 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R8-550 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R8-550-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R8-768 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R8-768-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain IRLM_2 16S ribosomal RNA gene, partial sequence
Bacterium GX11 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PA015 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PA006 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. NCCP-630 gene for 16S ribosomal RNA, partial sequence
Pseudomonas aeruginosa strain MB I-3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R25 16S ribosomal RNA gene, partial sequence
Bacterium GX12 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-764 16S ribosomal RNA gene, partial sequence
Bacterium GX9 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R6-357 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PA016 16S ribosomal RNA gene, partial sequence
0.0002

Leclercia adecarboxylata **KT899848.1**

Leclercia adecarboxylata strain MCCB 331 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT899848.1| **Length:** 1323 **Number of Matches:** 1

Range 1: 1 to 905 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1597 bits(1770)	0.0	897/905(99%)	1/905(0%)	Plus/Plus

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Query  6    GACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC  65
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Sbjct  1    GACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC  60

Query  66   TGGAAACGGTAGCTAATACCGCATAAYGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCT  125
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61   TGGAAACGGTAGCTAATACCGCATAATGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCT  120

Query  126  CTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGG  185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTGCCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGG  180

Query  186  CGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCA  245
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Sbjct  181  CGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCA  240

Query  246  GACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCC  305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCC  300

Query  306  ATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGAGGAGGAAGGCA  365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGAGGAGGAAGGCG  360

Query  366  TTGTGGTTAATAACCGCAGTGATTGACGTTACTCGCAGAAGAAGCACCGGCTAACTCCGT  425
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Sbjct  361  TTGTGGTTAATAACCACAGTGATTGACGTTACTCGCAGAAGAAGCACCGGCTAACTCCGT  420

Query  426  GCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGC  485
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Sbjct  421  GCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGC  480

Query  486  GCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCAT  545
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Sbjct  481  GCACGCAGGCGGTCTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCAT  540

Query  546  TTGAAACTGGCAGGCTTGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA  605
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Sbjct  541  TTGAAACTGGCAGGCTTGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAA  600

Query  606  TGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGC  665
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Sbjct  601  TGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGC  660

Query  666  TCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA  725
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  TCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA  720

Query  726  CGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTC  785
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  CGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTC  780

Query  786  GACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCG-CA  844
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  781  GACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCCA  840

Query  845  CAAGCGGGGGAGCATGTGGTTTAATTCAATGCAACGCGAAAAACCTTACCTACTCTTGAC  904
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Sbjct  841  CAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTRCTCTTGAC  900

Query  905  ATCCA  909
            |||||
Sbjct  901  ATCCA  905
```


Enterobacter sp. MT20 partial 16S rRNA gene, strain MT20
enterobacteria | 2 leaves
Enterobacter ludwigii strain VVS01-S1 16S ribosomal RNA gene, partial sequence
enterobacteria | 3 leaves
enterobacteria | 2 leaves
Enterobacter sp. ECU1107 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone NTV-Gly.P017 16S ribosomal RNA gene, partial sequence
enterobacteria | 3 leaves
Enterobacter ludwigii strain GM7 16S ribosomal RNA, partial sequence
Enterobacter asburiae strain RS01_04 16S ribosomal RNA gene, partial sequence
Bacterium strain RLF2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 218002-223 16S ribosomal RNA gene, partial sequence
Enterobacter hormaechei strain SPP-10 16S ribosomal RNA gene, partial sequence
Enterobacter sp. 1FTM7 16S ribosomal RNA gene, partial sequence
Enterobacter cloacae complex 'Hoffmann cluster IV' strain DSM 16690, complete genome
Enterobacter asburiae strain CAV1043, complete genome
Uncultured bacterium clone 218002-383 16S ribosomal RNA gene, partial sequence
enterobacteria | 2 leaves
enterobacteria | 9 leaves
Citrobacter sp. XT-10 16S ribosomal RNA gene, partial sequence
Enterobacter ludwigii strain CaR 16S ribosomal RNA gene, partial sequence
enterobacteria | 2 leaves
Enterobacter sp. 2V5B 16S ribosomal RNA gene, partial sequence
Enterobacter kobei partial 16S rRNA gene, strain DSM 13645T, clone 2
Leclercia sp. RF042 16S ribosomal RNA gene, complete sequence
Uncultured bacterium clone LB1B7 16S small subunit ribosomal RNA gene, partial sequence
enterobacteria | 4 leaves
Enterobacter sp. UIWRF0389 16S ribosomal RNA gene, partial sequence
Enterobacter sp. A16-1 gene for 16S rRNA, partial sequence, strain: A16-1
Leclercia adecarboxylata strain EPCC5 16S ribosomal RNA gene, partial sequence
Leclercia sp. 1185/07 16S ribosomal RNA gene, partial sequence
Leclercia sp. Z1-2-1 16S ribosomal RNA gene, partial sequence
Pantoea sp. PE4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2.1 16S ribosomal RNA gene, partial sequence
Leclercia sp. UPMLH2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone N4.6 16S ribosomal RNA gene, partial sequence
Enterobacter sp. BISR-TS27 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 0-172 16S ribosomal RNA gene, partial sequence
enterobacteria | 2 leaves
Uncultured bacterium clone ncd2317d04c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone X807 16S ribosomal RNA gene, partial sequence
Enterobacter cancerogenus strain BH4 16S ribosomal RNA gene, partial sequence
Enterobacter cloacae strain C3 16S ribosomal RNA gene, partial sequence
Bacterium OX_V1 16S ribosomal RNA gene, partial sequence
Enterobacteriaceae bacterium strain FGI 57, complete genome
Enterobacter amnigenus isolate 2 16S ribosomal RNA gene, partial sequence
Enterobacter sp. LBA3 16S ribosomal RNA gene, partial sequence
Enterobacter sp. TM1_3 16S ribosomal RNA gene, partial sequence
Enterobacter sp. TM1_4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone s4w5a 16S ribosomal RNA gene, partial sequence
enterobacteria | 4 leaves
enterobacteria | 3 leaves
enterobacteria | 7 leaves
Uncultured bacterium clone 7-53 16S ribosomal RNA gene, partial sequence
enterobacteria | 3 leaves
Enterobacteriaceae bacterium C3(2013) strain C3 16S ribosomal RNA gene, partial sequence
Enterobacter sp. N063 16S ribosomal RNA gene, partial sequence
Pantoea agglomerans partial 16S rRNA gene, strain WAB1951
Uncultured bacterium clone 5s9 16S ribosomal RNA gene, partial sequence
Enterobacter ludwigii strain A-B11B 16S ribosomal RNA gene, partial sequence
Enterobacter ludwigii strain N1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B2B2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B4B1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B4B2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B5W 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone W1B1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone W2B2 16S ribosomal RNA gene, partial sequence
Enterobacter sp. Yuan3 16S ribosomal RNA gene, partial sequence
0.003

Enterobacter asburiae **EU239468.1**

Enterobacter asburiae strain XJUHX-5 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|EU239468.1| **Length:** 1446 **Number of Matches:** 1

Range 1: 504 to 1394 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1573 bits(1744)	0.0	884/891(99%)	1/891(0%)	Plus/Minus

```
Query  1     TTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCAC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1394  TTTGCAACCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCAC  1335

Query  61    CGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1334  CGTAGCATTCTGATCTACGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACT  1275

Query  121   CCAATCCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1274  CCAATCCGGACTACGACGCACTTTATGAGGTCCGCTTGCTCTCGCGAGGTCGCTTCTCTT  1215

Query  181   TGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1214  TGTATGCGCCATTGTAGCACGTGTGTAGCCCTACTCGTAAGGGCCATGATGACTTGACGT  1155

Query  241   CATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCTAACCGC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1154  CATCCCCACCTTCCTCCAGTTTATCACTGGCAGTCTCCTTTGAGTTCCCGGCCTAACCGC  1095

Query  301   TGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1094  TGGCAACAAAGGATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATTTCACAACACG  1035

Query  361   AGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAAGCCATCTCTG  420
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  1034  AGCTGACGACAGCCATGCAGCACCTGTCTCAGAGTTCCCGAAGGCACCAATCCATCTCTG  975

Query  421   GCAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCAC  480
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  974   GAAAGTTCTCTGGATGTCAAGAGTAGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCAC  915

Query  481   ATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  914   ATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCATTTGAGTTTTAACCTTGCGGCCGTA  855

Query  541   CTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  854   CTCCCCAGGCGGTCGACTTAACGCGTTAGCTCCGGAAGCCACGCCTCAAGGGCACAACCT  795

Query  601   CCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  794   CCAAGTCGACATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCAC  735

Query  661   GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  734   GCTTTCGCACCTGAGCGTCAGTCTTTGTCCAGGGGGCCGCCTTCGCCACCGGTATTCCTC  675

Query  721   CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCAAG  780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  674   CAGATCTCTACGCATTTCACCGCTACACCTGGAATTCTACCCCCCTCTACAAGACTCTAG  615

Query  781   CCTGCCAGTTTCAAATGCAGTTCCC-NGTTGAGCCCGGGGATTTCACATCTGACTTAACA  839
             |||||||||||| |||||||||||   |||||||||||||||||||||||||||| |||
Sbjct  614   CCTGCCAGTTTCGAATGCAGTTCCCAGGTTGAGCCCGGGGATTTCACATCTGACTTGACA  555

Query  840   GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCC  890
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554   GACCGCCTGCGTGCGCTTTACGCCCAGTAATTCCGATTAACGCTTGCACCC  504
```


Uncultured bacterium clone czt23 16S ribosomal RNA gene, partial sequence
kl|Query_237153
Leclercia sp. 1185107 16S ribosomal RNA gene, partial sequence
Leclercia sp. Z1-2-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone X807 16S ribosomal RNA gene, partial sequence
Enterobacter sp. GNTEW-13-11 16S ribosomal RNA gene, partial sequence
Leclercia sp. UPMLH2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2.3 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 0-172 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 4.10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone N4.6 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 2.1 16S ribosomal RNA gene, partial sequence
Enterobacter sp. BISR-TS27 16S ribosomal RNA gene, partial sequence
enterobacteria | 2 leaves
enterobacteria | 4 leaves
enterobacteria | 2 leaves
enterobacteria | 3 leaves
Rhizobium sp. BGC8 16S ribosomal RNA gene, partial sequence
Pantoea agglomerans strain A9 16S ribosomal RNA gene, partial sequence
Enterobacter sp. E20, complete genome
Leclercia adecarboxylata strain CIP 82.92 16S ribosomal RNA gene, partial sequence
Leclercia adecarboxylata strain I1 5 16S ribosomal RNA gene, partial sequence
Enterobacter sp. RCB183 16S ribosomal RNA gene, partial sequence
Enterobacter sp. RCB182 16S ribosomal RNA gene, partial sequence
Enterobacter sp. IFC1-8 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0760 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0752 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0359 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0222 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF1339 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0968 16S ribosomal RNA gene, partial sequence
Cedecea davisae strain BCG10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium isolate DGGE gel band clone 14 16S ribosomal RNA gene, partial sequence
Enterobacter asburiae strain CAV1043, complete genome
Enterobacter sp. NGB-FR110 gene for 16S ribosomal RNA, partial sequence
Enterobacter sp. NGB-FR109 gene for 16S ribosomal RNA, partial sequence
Enterobacter sp. NGB-FR98 gene for 16S ribosomal RNA, partial sequence
Enterobacter cloacae strain HNR 16S ribosomal RNA gene, partial sequence
Enterobacter asburiae strain pca3 16S ribosomal RNA gene, partial sequence
Enterobacter sp. YJY1 16S ribosomal RNA gene, partial sequence
Uncultured prokaryote clone seq_G01_Z0161_Z001162a_X-L21_16SR 16S ribosomal RNA gene, partial sequence
Uncultured prokaryote clone seq_T-S6_16SR 16S ribosomal RNA gene, partial sequence
Uncultured prokaryote clone seq_T-S4T_16SR 16S ribosomal RNA gene, partial sequence
Uncultured Enterobacter sp. clone ND2 16S ribosomal RNA gene, partial sequence
Enterobacter cancerogenus strain g5 16S ribosomal RNA gene, partial sequence
Enterobacter cloacae strain B193-3 16S ribosomal RNA gene, partial sequence
Enterobacter cloacae strain ATCC 39978 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R2W 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R2B2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R2B1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R1B2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R1W 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone R1B1 16S ribosomal RNA gene, partial sequence
Enterobacter ludwigii strain ALS-2 16S ribosomal RNA gene, partial sequence
Enterobacter aerogenes strain K3-9 16S ribosomal RNA gene, partial sequence
Enterobacter aerogenes strain K3-2 16S ribosomal RNA gene, partial sequence
Enterobacter asburiae strain S-X11A 16S ribosomal RNA gene, partial sequence
Leclercia adecarboxylata strain M-X17B 16S ribosomal RNA gene, partial sequence
Leclercia adecarboxylata strain A-X9A 16S ribosomal RNA gene, partial sequence
Enterobacter asburiae strain ITM 1512 16S ribosomal RNA gene, partial sequence
Enterobacter sp. XBGRY6 16S ribosomal RNA gene, partial sequence
Enterobacter sp. XBGRY1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 218002-5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 218002-1-61 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 218002-19 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 218002-1-57 16S ribosomal RNA gene, partial sequence
Uncultured Enterobacter sp. clone JU-S2A2 16S ribosomal RNA gene, partial sequence
Enterobacter asburiae strain m-4 16S ribosomal RNA gene, partial sequence
Enterobacter ludwigii strain IHB B 6551 16S ribosomal RNA gene, partial sequence
Enterobacter aerogenes strain P5 16S ribosomal RNA gene, partial sequence
Enterobacter aerogenes strain XF15 16S ribosomal RNA gene, partial sequence
Enterobacter cloacae subsp. dissolvens strain SB 3013 16S ribosomal RNA gene, partial sequence
Bacterium BM0593 16S ribosomal RNA gene, partial sequence
enterobacteria | 8 leaves
enterobacteria | 10 leaves

Candidatus Roseomonas massiliae KT321690.1

Candidatus Roseomonas massiliae 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT321690.1| **Length:** 1443 **Number of Matches:** 1

Range 1: 74 to 974 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1613 bits(1788)	0.0	898/901(99%)	0/901(0%)	Plus/Plus

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Query  1    GGACGGGTGAGTAACGCGTAGGAACGTGTCCTGAGGTGGGGGACAACCCCGGGAAACTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   GGACGGGTGAGTAACGCGTAGGAACGTGTCCTGAGGTGGGGGACAACCCCGGGAAACTGG  133

Query  61   GGCTAATACCGCATATGGGCTGAGGCCCAAAGCCGAGAGGCGCCTTTGGAGCGGCCTGCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  GGCTAATACCGCATATGGGCTGAGGCCCAAAGCCGAGAGGCGCCTTTGGAGCGGCCTGCG  193

Query  121  TCCGATTAGGTAGTTGGTGGGGTAAAGGCCTACCAAGCCTGCGATCGGTAGCTGGTCTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  TCCGATTAGGTAGTTGGTGGGGTAAAGGCCTACCAAGCCTGCGATCGGTAGCTGGTCTGA  253

Query  181  GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGT  313

Query  241  GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGGGTGAAGAAGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  GGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGGGTGAAGAAGGT  373

Query  301  CTTCGGATCGTAAAGCCCTTTCGACGGGGACGATGATGACGGTACCCGTAGAAGAAGCCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  CTTCGGATCGTAAAGCCCTTTCGACGGGGACGATGATGACGGTACCCGTAGAAGAAGCCC  433

Query  361  CGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434  CGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATTA  493

Query  421  CTGGGCGTAAAGGGCGCGTAGGCGGCGGCCCAAGTCAGGCGTGAAATTCCTGGGCTCAAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  494  CTGGGCGTAAAGGGCGCGTAGGCGGCGGCCCAAGTCAGGCGTGAAATTCCTGGGCTCAAC  553

Query  481  CTGGGGACTGCGCTTGATACTGGGTTGCTTGAGGATGGAAGAGGCTCGTGGAATTCCCAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554  CTGGGGACTGCGCTTGATACTGGGTTGCTTGAGGATGGAAGAGGCTCGTGGAATTCCCAG  613

Query  541  TGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCGAGCTGGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  614  TGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCGAGCTGGT  673

Query  601  CCATTACTGACGCTGAGGCGCGACAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  674  CCATTACTGACGCTGAGGCGCGACAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG  733

Query  661  TCCACGCCGTAAACGATGTGCGCTGGATGTTGGGGCCCATAGGGTCTCAGTGTCGTAGCC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  734  TCCACGCCGTAAACGATGTGCGCTGGATGTTGGGGCCCATAGGGTCTCAGTGTCGTAGCC  793

Query  721  AACGCGGTAAGCGCACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  794  AACGCGGTAAGCGCACCGCCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGA  853

Query  781  CGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCANAACCTTA  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  854  CGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTA  913

Query  841  CCAGCCCTTGACATGGTCACGACCGGTCCAAAAATGGACTTTCCTAGCAATAGGCGTGAT  900
            |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Sbjct  914  CCAGCCCTTGACATGGTCACGACCGGTCCAGAGATGGACTTTCCTAGCAATAGGCGTGAT  973

Query  901  G  901
            |
Sbjct  974  G  974
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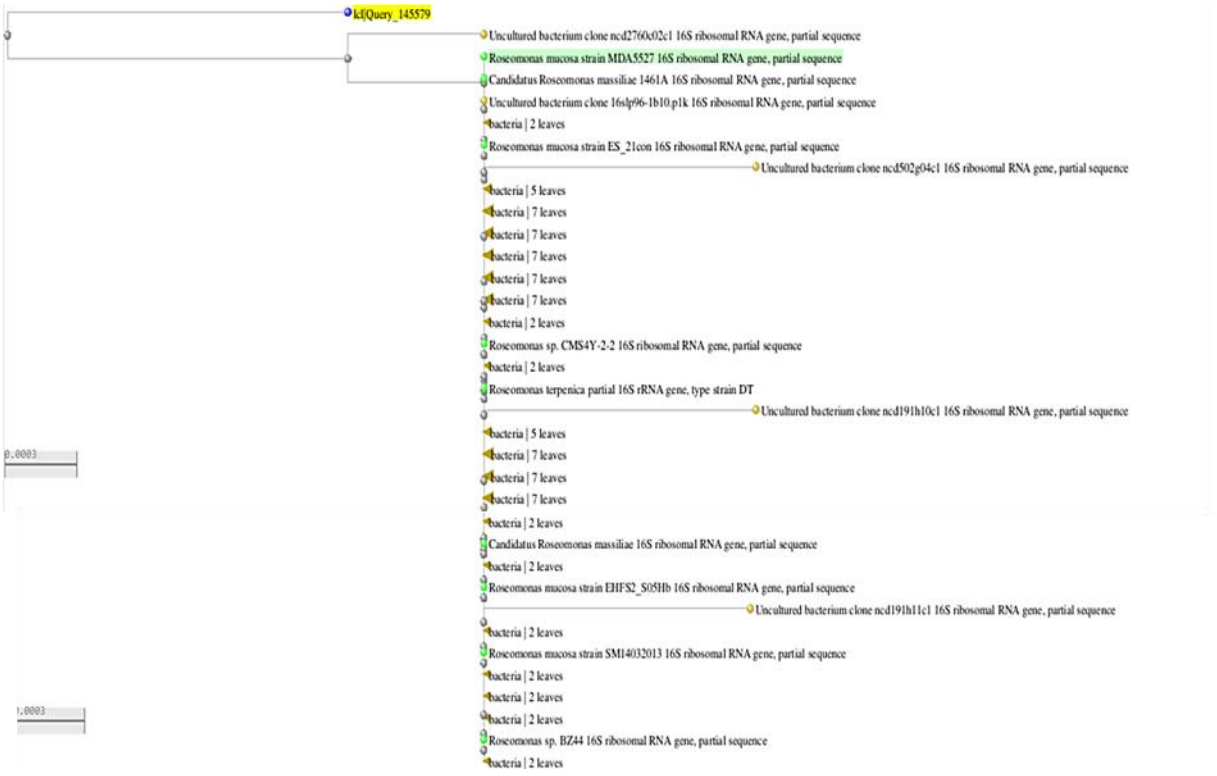
kl|Query_145579
Uncultured bacterium clone ncd2760x02c1 16S ribosomal RNA gene, partial sequence
Roseomonas mucosa strain MDA5527 16S ribosomal RNA gene, partial sequence
Candidatus Roseomonas massiliae 1461A 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 16slp96-1b10.p1k 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Roseomonas mucosa strain ES_21con 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd502g04c1 16S ribosomal RNA gene, partial sequence
bacteria | 5 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 2 leaves
Roseomonas sp. CMS4Y-2-2 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Roseomonas terpenica partial 16S rRNA gene, type strain DT
Uncultured bacterium clone ncd191h10c1 16S ribosomal RNA gene, partial sequence
bacteria | 5 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 7 leaves
bacteria | 2 leaves
Candidatus Roseomonas massiliae 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Roseomonas mucosa strain EHFS2_S05Hb 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd191h11c1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
Roseomonas mucosa strain SMI4032013 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
bacteria | 2 leaves
bacteria | 2 leaves
Roseomonas sp. BZ44 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves

Pseudomonas parafulva KT758848.1

Pseudomonas parafulva strain YAB-1 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KT758848.1| **Length:** 1401 **Number of Matches:** 1

Range 1: 39 to 980 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
1651 bits(1830)	0.0	933/942(99%)	2/942(0%)	Plus/Plus

```
Query  1    AGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  39   AGCGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTTTCGA  98

Query  61   AAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  99   AAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCG  158

Query  121  CTATCAGATGAGCCTAGGTCGGATTAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  159  CTATCAGATGAGCCTAGGTCGGATTAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGAC  218

Query  181  GATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  219  GATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACT  278

Query  241  CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  279  CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGC  338

Query  301  CGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  339  CGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTA  398

Query  361  GATTAATACTCTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  399  GATTAATACTCTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCA  458

Query  421  GCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  459  GCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGC  518

Query  481  GTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519  GTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAA  578

Query  541  AACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  579  AACTGGCAAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCG  638

Query  601  TAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  639  TAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAG  698

Query  661  GTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGAT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  699  GTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGAT  758

Query  721  GTCAACTAGCCGTTGGAATCCTTGAGATTTTAGTGGCGCAGCTAACGCATTAAGTTGACC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  759  GTCAACTAGCCGTTGGAATCCTTGAGATTTTAGTGGCGCAGCTAACGCATTAAGTTGACC  818

Query  781  GCCTGGGGAGTACGGCCGCAAGGTT-AAACTCAAATGAATTGACGGGGGCCCGCACAAGC  839
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  819  GCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGC  878

Query  840  GGTGGAGCATGTGGTTTAATTCGAAACAACGCGAAAAACCTTACCAGGCCTTGACATGCA  899
            ||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||
Sbjct  879  GGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATGCA  938

Query  900  AAAAACTTTCCAAAAATGGATTGGGGCCTTCGGG-ACTCTGA  940
              | ||||||||| | ||||||||| ||||||||| |||||||
Sbjct  939  GAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGA  980
```


Pseudomonas sp. 4 16S ribosomal RNA gene, partial sequence
Pseudomonas parafulva strain AJ 2129 16S ribosomal RNA gene, partial sequence
Pseudomonas parafulva strain AJ 2129 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. Fa24 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2626a08c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain EX4 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain CLF2014-1 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
g-proteobacteria | 4 leaves
Pseudomonas fulva strain 1Y1103 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nbw621f12c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain i7_MX 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. DP108 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. NCCP-562 gene for 16S ribosomal RNA, partial sequence
bacteria | 2 leaves
Pseudomonas sp. NCCP-553 gene for 16S ribosomal RNA, partial sequence
Uncultured bacterium clone nbt18d11 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain i13_MX 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 4 leaves
Pseudomonas fulva gene for 16S rRNA, partial sequence, strain: NBRC 16638
Pseudomonas fulva 67 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck137a07c1 16S ribosomal RNA gene, partial sequence
Endophytic bacterium SV807 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. NCCP-571 gene for 16S ribosomal RNA, partial sequence
Pseudomonas sp. NLW-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2661h11c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain SW32 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain iMX35 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 654955 16S ribosomal RNA gene, partial sequence
Pseudomonas parafulva strain L4-302 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain AKB22 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain ANA72 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. ANA71 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd905h11c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva partial 16S rRNA gene, strain YMC09/4/B4619
Pseudomonas parafulva strain NBRC 16636 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2803c07c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. MH-135 16S rRNA gene, strain MH-135
Pseudomonas fulva strain BSW6 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. enrichment culture clone 8 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. 3zhy partial 16S rRNA gene, strain 3zhy
Uncultured bacterium clone ncd2564f11c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. MG-2011-7-BJ partial 16S rRNA gene, strain 7, isolate BJ
Uncultured bacterium clone nbt22b10 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain iP1_MX 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. DP109B 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. NCCP-561 gene for 16S ribosomal RNA, partial sequence
Pseudomonas sp. 2B5B 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone MWL-15 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone nck137d02c1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. URMO17WK12:I11 genome assembly YEL.embl.gz, chromosome : 1
Pseudomonas parafulva strain CRS01-1, complete genome
Pseudomonas sp. LB-X-GYM-4-1 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. LB-S-GYM-2 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2686h02c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain BSW3 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. B-6 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. H10zhy partial 16S rRNA gene, strain H10zhy
Uncultured bacterium clone ncd861g02c1 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 6 leaves
Pseudomonas fulva strain SGRAJ09 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2598e06c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain QC07 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain BSW1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva partial 16S rRNA gene, strain Zb7zhy
Uncultured bacterium clone ncd908e02c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva gene for 16S rRNA, partial sequence, strain: NBRC 16639
Uncultured bacterium clone nbw643d01c1 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain i19_MX 16S ribosomal RNA gene, partial sequence
Bacterium AM0315 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. NCCP-567 gene for 16S ribosomal RNA, partial sequence
Pseudomonas sp. 471-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2670f06c1 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain JT-K21 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone Cal07 74
d-proteobacteria | 4 leaves
e-proteobacteria | 3 leaves
Pseudomonas fulva strain BSW8 16S ribosomal RNA gene, partial sequence
Pseudomonas fulva strain Cl-11 16S ribosomal RNA gene, partial sequence
Pseudomonas putida strain F29 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2625e06c1 16S ribosomal RNA gene, partial sequence

Bacillus licheniformis KU314515.1

Bacillus licheniformis strain HS10 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KU314515.1| **Length:** 1514 **Number of Matches:** 1

Range 1: 491 to 1441 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1710 bits(1896)	0.0	950/951(99%)	0/951(0%)	Plus/Minus

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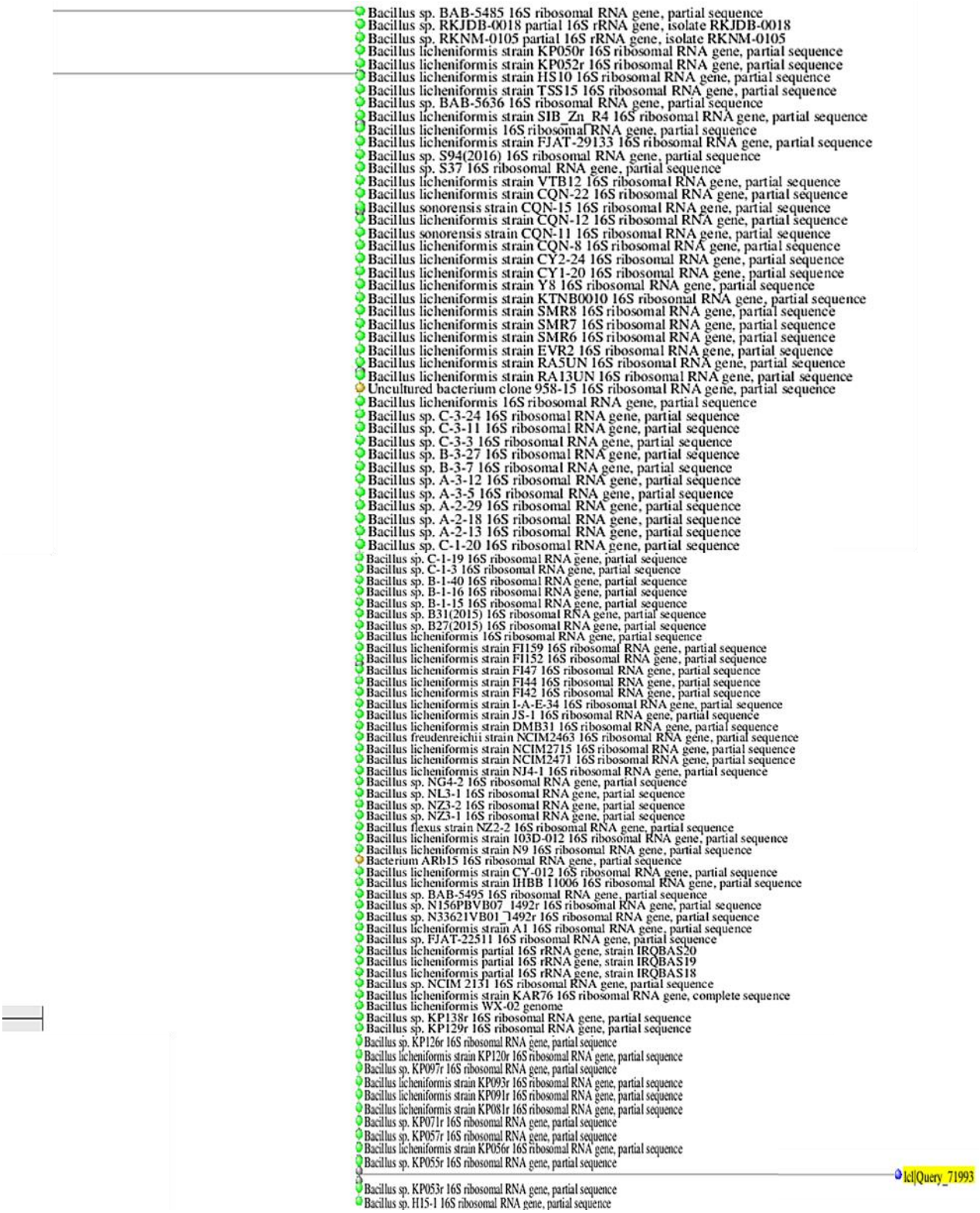
Bacillus sp. BAB-5485 16S ribosomal RNA gene, partial sequence
Bacillus sp. RKJDB-0018 partial 16S rRNA gene, isolate RKJDB-0018
Bacillus sp. RKNM-0105 partial 16S rRNA gene, isolate RKNM-0105
Bacillus licheniformis strain KP050r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP052r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain HS10 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain TSS15 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5636 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SIB_Zn_R4 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FJAT-29133 16S ribosomal RNA gene, partial sequence
Bacillus sp. S94(2016) 16S ribosomal RNA gene, partial sequence
Bacillus sp. S37 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain VTB12 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CQN-22 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain CQN-15 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CQN-12 16S ribosomal RNA gene, partial sequence
Bacillus sonorensis strain CQN-11 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CQN-8 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CY2-24 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CY1-20 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain Y8 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KTNB0010 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SMR8 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SMR7 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain SMR6 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain EVR2 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain RA5UN 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain RA13UN 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 958-15 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-3-24 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-3-11 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-3-3 16S ribosomal RNA gene, partial sequence
Bacillus sp. B-3-27 16S ribosomal RNA gene, partial sequence
Bacillus sp. B-3-7 16S ribosomal RNA gene, partial sequence
Bacillus sp. A-3-12 16S ribosomal RNA gene, partial sequence
Bacillus sp. A-3-5 16S ribosomal RNA gene, partial sequence
Bacillus sp. A-2-29 16S ribosomal RNA gene, partial sequence
Bacillus sp. A-2-18 16S ribosomal RNA gene, partial sequence
Bacillus sp. A-2-13 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-1-20 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-1-19 16S ribosomal RNA gene, partial sequence
Bacillus sp. C-1-3 16S ribosomal RNA gene, partial sequence
Bacillus sp. B-1-40 16S ribosomal RNA gene, partial sequence
Bacillus sp. B-1-16 16S ribosomal RNA gene, partial sequence
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Bacillus sp. B31(2015) 16S ribosomal RNA gene, partial sequence
Bacillus sp. B27(2015) 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI159 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain FI152 16S ribosomal RNA gene, partial sequence
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Bacillus licheniformis strain FI42 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain I-A-E-34 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain JS-1 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain DMB31 16S ribosomal RNA gene, partial sequence
Bacillus freudenreichii strain NCIM2463 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NCIM2715 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain NCIM2471 16S ribosomal RNA gene, partial sequence
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Bacillus sp. NZ3-2 16S ribosomal RNA gene, partial sequence
Bacillus sp. NZ3-1 16S ribosomal RNA gene, partial sequence
Bacillus flexus strain NZ2-2 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain 103D-012 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain N9 16S ribosomal RNA gene, partial sequence
Bacterium ARb15 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain CY-012 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain IHBB 11006 16S ribosomal RNA gene, partial sequence
Bacillus sp. BAB-5495 16S ribosomal RNA gene, partial sequence
Bacillus sp. N156PBVB07_1492r 16S ribosomal RNA gene, partial sequence
Bacillus sp. N33621VB01_1492r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain A1 16S ribosomal RNA gene, partial sequence
Bacillus sp. FJAT-22511 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS20
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS19
Bacillus licheniformis partial 16S rRNA gene, strain IRQBAS18
Bacillus sp. NCIM 2131 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KAR76 16S ribosomal RNA gene, complete sequence
Bacillus licheniformis WX-02 genome
Bacillus sp. KP138r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP129r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP126r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP120r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP097r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP093r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP091r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP081r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP071r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP057r 16S ribosomal RNA gene, partial sequence
Bacillus licheniformis strain KP056r 16S ribosomal RNA gene, partial sequence
Bacillus sp. KP055r 16S ribosomal RNA gene, partial sequence
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Bacillus sp. KP053r 16S ribosomal RNA gene, partial sequence
Bacillus sp. H15-1 16S ribosomal RNA gene, partial sequence

Pseudomonas aeruginosa KF680991.1

Pseudomonas aeruginosa strain ATHA23 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF680991.1| **Length:** 1115 **Number of Matches:** 1

Range 1: 86 to 1065 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
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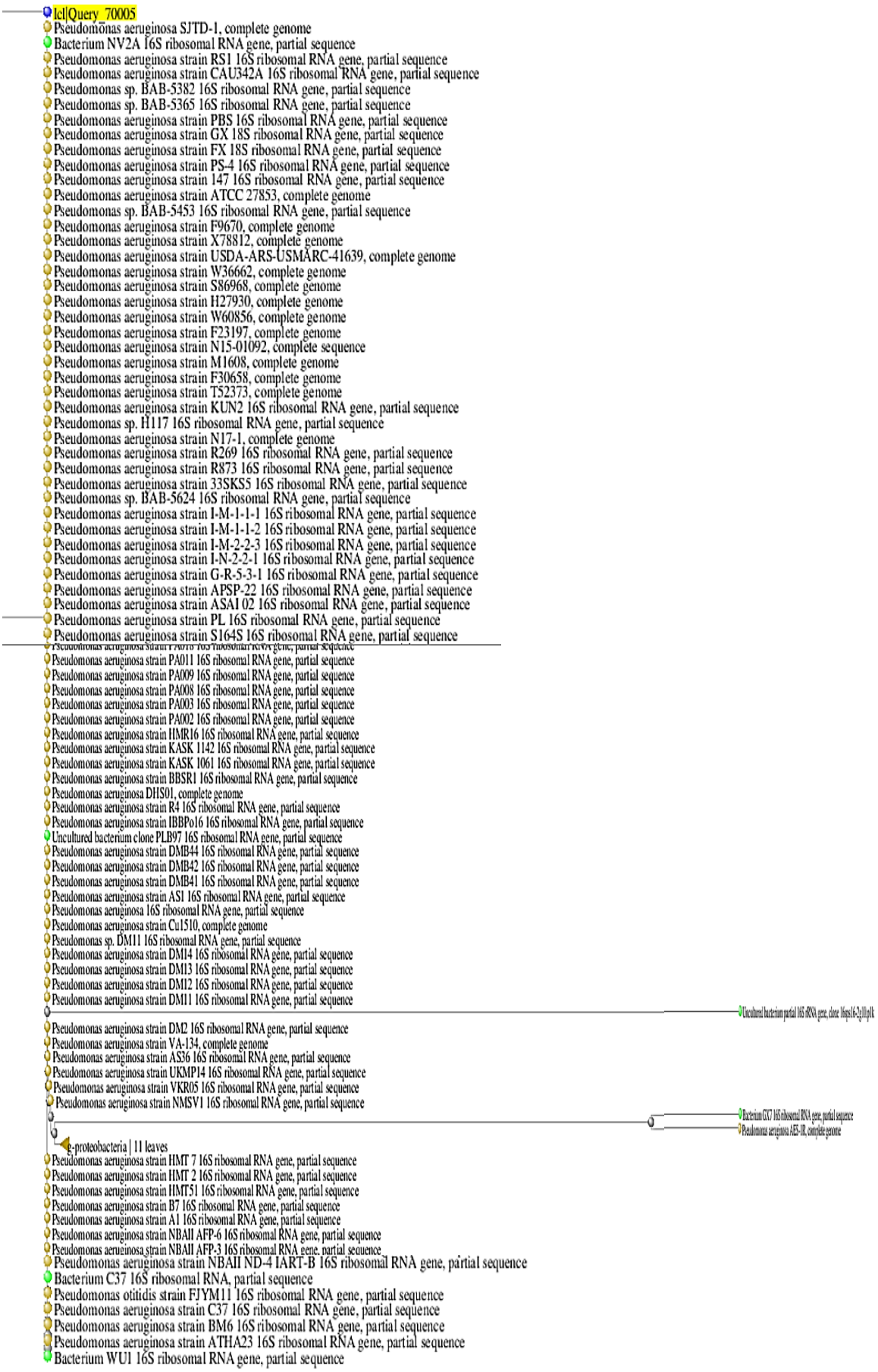
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Pseudomonas aeruginosa SJTD-1, complete genome
Bacterium NV2A 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain RS1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain CAU342A 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. BAB-5382 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. BAB-5365 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PBS 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain GX 18S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain FX 18S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PS-4 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 147 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ATCC 27853, complete genome
Pseudomonas sp. BAB-5453 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain F9670, complete genome
Pseudomonas aeruginosa strain X78812, complete genome
Pseudomonas aeruginosa strain USDA-ARS-USMARC-41639, complete genome
Pseudomonas aeruginosa strain W36662, complete genome
Pseudomonas aeruginosa strain S86968, complete genome
Pseudomonas aeruginosa strain H27930, complete genome
Pseudomonas aeruginosa strain W60856, complete genome
Pseudomonas aeruginosa strain F23197, complete genome
Pseudomonas aeruginosa strain N15-01092, complete sequence
Pseudomonas aeruginosa strain M1608, complete genome
Pseudomonas aeruginosa strain F30658, complete genome
Pseudomonas aeruginosa strain T52373, complete genome
Pseudomonas aeruginosa strain KUN2 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. H117 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain N17-1, complete genome
Pseudomonas aeruginosa strain R269 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain R873 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain 33SKS5 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. BAB-5624 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I-M-1-1-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I-M-1-1-2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I-M-2-2-3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain I-N-2-2-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain G-R-5-3-1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain APSP-22 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ASAI 02 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PL 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain S164S 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PA011 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain PA009 16S ribosomal RNA gene, partial sequence
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Pseudomonas aeruginosa strain PA003 16S ribosomal RNA gene, partial sequence
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Pseudomonas aeruginosa strain HMR16 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain KASK 1142 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain KASK 1061 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BBSR1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa DHS01, complete genome
Pseudomonas aeruginosa strain R4 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain IBBPo16 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone PLB97 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DMB44 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DMB42 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DMB41 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain AS1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain Cu1510, complete genome
Pseudomonas sp. DM11 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DM14 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DM13 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DM12 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain DM11 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone Mspa16-2-11p1k
Pseudomonas aeruginosa strain DM2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain VA-134, complete genome
Pseudomonas aeruginosa strain AS36 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain UKMP14 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain VKR05 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NMSV1 16S ribosomal RNA gene, partial sequence
Bacterium GX7 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa AES-1R, complete genome
g-proteobacteria | 11 leaves
Pseudomonas aeruginosa strain HMT 7 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain HMT 2 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain HMT51 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain B7 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain A1 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NBAII AFP-6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NBAII AFP-3 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain NBAII ND-4 IART-B 16S ribosomal RNA gene, partial sequence
Bacterium C37 16S ribosomal RNA, partial sequence
Pseudomonas otitidis strain FJYM11 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain C37 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain BM6 16S ribosomal RNA gene, partial sequence
Pseudomonas aeruginosa strain ATHA23 16S ribosomal RNA gene, partial sequence
Bacterium WU1 16S ribosomal RNA gene, partial sequence

Agrobacterium larrymoorei EF178437.1

Agrobacterium larrymoorei strain 2R46 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|EF178437.1| **Length:** 1414 **Number of Matches:** 1

Range 1: 398 to 1329 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1676 bits(1858)	0.0	931/932(99%)	0/932(0%)	Plus/Minus

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Query  1     GGGTAAAACCAACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCA  60
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Sbjct  1329  GGGTAAAACCAACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCA  1270

Query  61    CCGCAGCATGCTGATCTGCGATTACTAGCGATTCCAACTTCATGCACTCGAGTTGCAGAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1269  CCGCAGCATGCTGATCTGCGATTACTAGCGATTCCAACTTCATGCACTCGAGTTGCAGAG  1210

Query  121   TGCAATCCGAACTGAGATGGCTTTTGGAGATTAGCTCGACATCGCTGTCTCGCTGCCCAC  180
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Sbjct  1209  TGCAATCCGAACTGAGATGGCTTTTGGAGATTAGCTCGACATCGCTGTCTCGCTGCCCAC  1150

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Sbjct  1149  TGTCACCACCATTGTAGCACGTGTGTAGCCCAGCCCGTAAGGGCCATGAGGACTTGACGT  1090

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Sbjct  1089  CATCCCCACCTTCCTCTCGGCTTATCACCGGCAGTCCCCTTAGAGTGCCCAACCAAATGC  1030

Query  301   TGGCAACTAAGGGCGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACG  360
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Sbjct  1029  TGGCAACTAAGGGCGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACG  970

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Sbjct  969   AGCTGACGACAGCCATGCAGCACCTGTTCTAGGGCCAGCCGAACTGAAGGTCATCGTCTC  910

Query  421   CAATGACCATACCCCGAATGTCAAGAGCTGGTAAGGTTCTGCGCGTTGCTTCGAATTAAA  480
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Sbjct  909   CAATGACCATACCCCGAATGTCAAGAGCTGGTAAGGTTCTGCGCGTTGCTTCGAATTAAA  850

Query  481   CCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGAC  540
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Sbjct  849   CCACATGCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTAATCTTGCGAC  790

Query  541   CGTACTCCCCAGGCGGAATGTTTAATGCGTTAGCTGCGCCACCGAACAGTATACTGCCCG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ast.ncbi.nlm.nih.gov/Blast.cgi#dlgDwnl_122892477 AATGTTTAATGCGTTAGCTGCGCCACCGAACAGTATACTGCCCG  730

Query  601   ACGGCTAACATTCATCGTTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCC  660
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Sbjct  669   CACGCTTTCGCACCTCAGCGTCAGTAATGGACCAGTAAGCCGCCTTCGCCACTGGTGTTC  610

Query  721   CTGCGAATATCTACGAATTTCACCTCTACACTCGCAATTCCACTTACCTCTTCCATACTC  780
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Sbjct  609   CTGCGAATATCTACGAATTTCACCTCTACACTCGCAATTCCACTTACCTCTTCCATACTC  550

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549   AAGATACCCAGTATCAAAGGCAGTTCCAGAGTTGAGCTCTGGGATTTCACCCCTGACTTA  490

Query  841   AATATCCGCCTACGTGCGCTTTACGCCCAGTAATTCCAAACAACGCTAGCCCCCTTCGTA  900
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  489   AATATCCGCCTACGTGCGCTTTACGCCCAGTAATTCCGAACAACGCTAGCCCCCTTCGTA  430

Query  901   TTACCGCGGCTGCTGGCACGAAGTTAGCCGGG  932
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Sbjct  429   TTACCGCGGCTGCTGGCACGAAGTTAGCCGGG  398
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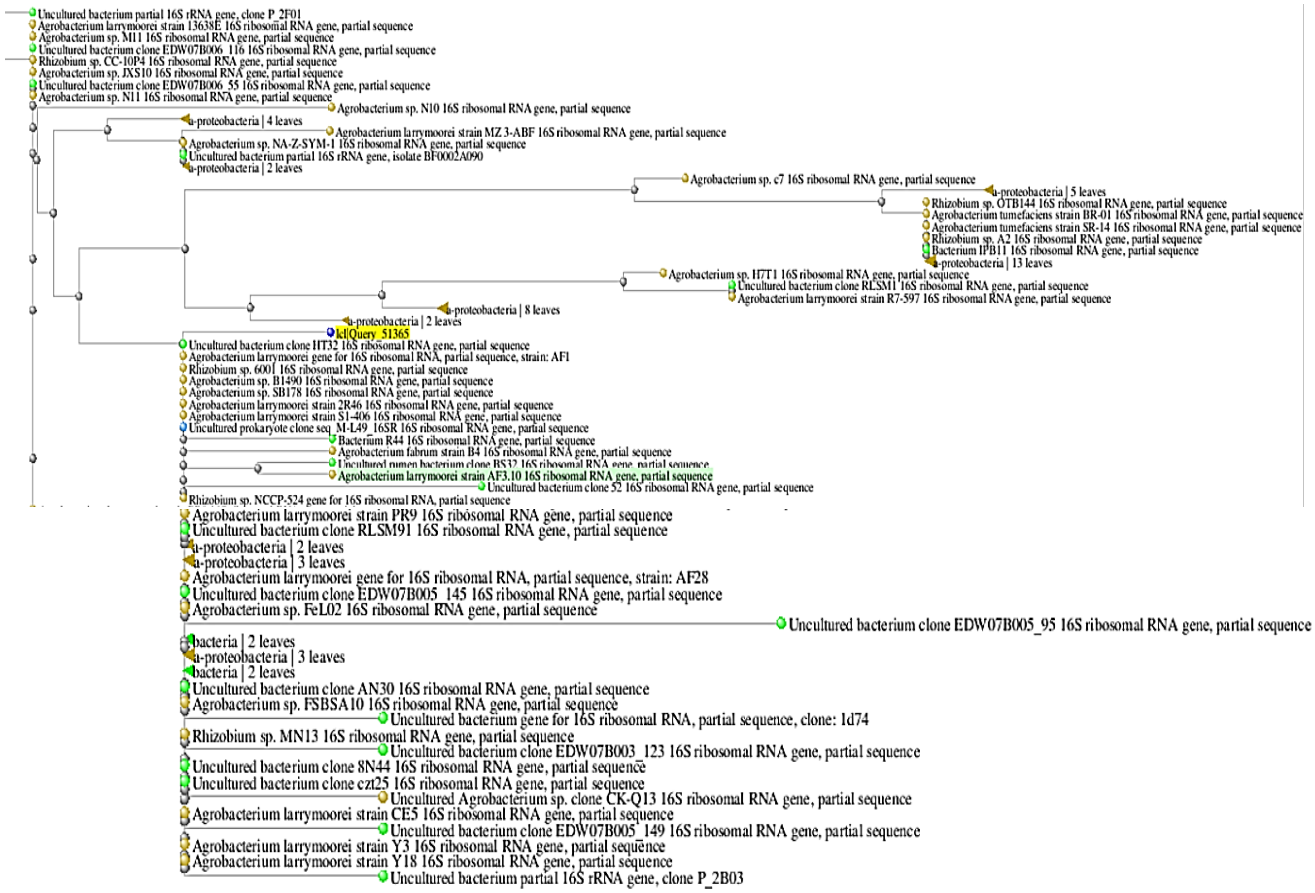
Uncultured bacterium partial 16S rRNA gene, clone P_2F01
Agrobacterium larrymoorei strain 13638E 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. M11 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone EDW07B006_116 16S ribosomal RNA gene, partial sequence
Rhizobium sp. CC-10P4 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. JX510 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone EDW07B006_55 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. N11 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. N10 16S ribosomal RNA gene, partial sequence
α-proteobacteria | 4 leaves
Agrobacterium larrymoorei strain MZ3-ABF 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. NA-Z-SYM-1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, isolate BF0002A090
α-proteobacteria | 2 leaves
Agrobacterium sp. c7 16S ribosomal RNA gene, partial sequence
α-proteobacteria | 5 leaves
Rhizobium sp. OTB144 16S ribosomal RNA gene, partial sequence
Agrobacterium tumefaciens strain BR-01 16S ribosomal RNA gene, partial sequence
Agrobacterium tumefaciens strain SR-14 16S ribosomal RNA gene, partial sequence
Rhizobium sp. A2 16S ribosomal RNA gene, partial sequence
Bacterium IPB11 16S ribosomal RNA gene, partial sequence
α-proteobacteria | 13 leaves
Agrobacterium sp. H7T1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone RLSM1 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain R7-597 16S ribosomal RNA gene, partial sequence
α-proteobacteria | 8 leaves
α-proteobacteria | 2 leaves
kl|Query_51365
Uncultured bacterium clone HT32 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei gene for 16S ribosomal RNA, partial sequence, strain: AF1
Rhizobium sp. 6001 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. H1490 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. SB178 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain 2R46 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain S1-406 16S ribosomal RNA gene, partial sequence
Uncultured prokaryote clone seq_M-L49_16SR 16S ribosomal RNA gene, partial sequence
Bacterium R44 16S ribosomal RNA gene, partial sequence
Agrobacterium fabrum strain B4 16S ribosomal RNA gene, partial sequence
Uncultured rumen bacterium clone RS37 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain AF3.10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 52 16S ribosomal RNA gene, partial sequence
Rhizobium sp. NCCP-524 gene for 16S ribosomal RNA, partial sequence
Agrobacterium larrymoorei strain PR9 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone RLSM91 16S ribosomal RNA gene, partial sequence
α-proteobacteria | 2 leaves
α-proteobacteria | 3 leaves
Agrobacterium larrymoorei gene for 16S ribosomal RNA, partial sequence, strain: AF28
Uncultured bacterium clone EDW07B005_145 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. FeL02 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone EDW07B005_95 16S ribosomal RNA gene, partial sequence
bacteria | 2 leaves
α-proteobacteria | 3 leaves
bacteria | 2 leaves
Uncultured bacterium clone AN30 16S ribosomal RNA gene, partial sequence
Agrobacterium sp. FSBSA10 16S ribosomal RNA gene, partial sequence
Uncultured bacterium gene for 16S ribosomal RNA, partial sequence, clone: Id74
Rhizobium sp. MN13 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone EDW07B003_123 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 8N44 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone czt25 16S ribosomal RNA gene, partial sequence
Uncultured Agrobacterium sp. clone CK-Q13 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain CE5 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone EDW07B005_149 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain Y3 16S ribosomal RNA gene, partial sequence
Agrobacterium larrymoorei strain Y18 16S ribosomal RNA gene, partial sequence
Uncultured bacterium partial 16S rRNA gene, clone P_2B03

Pantoea septica KF475883.1

Pantoea septica strain IHB B 1545 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KF475883.1| **Length:** 1508 **Number of Matches:** 1

Range 1: 68 to 975 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1599 bits(1772)	0.0	900/908(99%)	1/908(0%)	Plus/Plus

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Query  1    ACAGAAGAGCTTGCTCTTTGGGTGGCGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACT  60
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Sbjct  68   ACAGAAGAGCTTGCTCTTTGGGTGGCGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACT  127

Query  61   GCCCGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGAC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  128  GCCCGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGAC  187

Query  121  CAAAGTGGGGGACCTTCGGGCCTCACACCATCGGATGTGCCCAGATGGGATTAGCTAGTA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  188  CAAAGTGGGGGACCTTCGGGCCTCACACCATCGGATGTGCCCAGATGGGATTAGCTAGTA  247

Query  181  GGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCA  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  GGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCA  307

Query  241  CACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACA  300
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Sbjct  308  CACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACA  367

Query  301  ATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAG  360
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Sbjct  368  ATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAG  427

Query  361  TACTTTCAGCGGGGAGGAAGGCGACGCGGTTAATAACCGCGTCGATTGACGTTACCCGCA  420
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Sbjct  428  TACTTTCAGCGGGGAGGAAGGCGACGCGGTTAATAGCCGCGTCGATTGACGTTACCCGCA  487

Query  421  GAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTA  480
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Sbjct  488  GAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTA  547

Query  481  ATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCC  540
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Sbjct  548  ATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCC  607

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Sbjct  608  CGGGCTTAACCTGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTA  667

Query  601  GAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCG  660
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Sbjct  668  GAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCG  727

Query  661  GCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAT  720
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Sbjct  728  GCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAT  787

Query  721  ACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGCTGTTCCCCTGAGGAGTGGC  780
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Sbjct  788  ACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGCTGTTCCCTTGAGAAGTGGC  847

Query  781  TTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGGCGCAAGGTTAAAACTCA  840
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  848  TTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCA  907

Query  841  AATGAATTGACGGGGGCCCGCCCAAGCGGGGGAGCATGTGGTTTAATTCGATGC-ACGCG  899
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Sbjct  908  AATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCG  967

Query  900  AAAAACCT  907
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Sbjct  968  AAGAACCT  975
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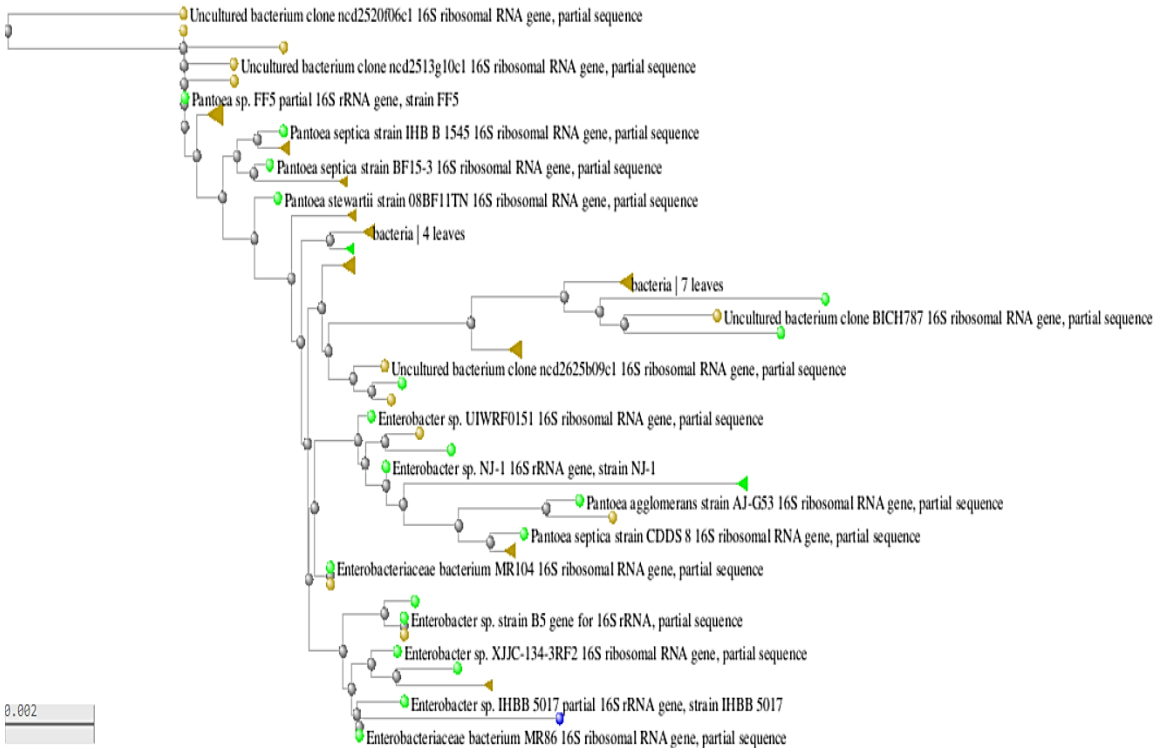
Uncultured bacterium clone ncd2520f06c1 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2513g10c1 16S ribosomal RNA gene, partial sequence
Pantoea sp. FF5 partial 16S rRNA gene, strain FF5
Pantoea septica strain IHB B 1545 16S ribosomal RNA gene, partial sequence
Pantoea septica strain BF15-3 16S ribosomal RNA gene, partial sequence
Pantoea stewartii strain 08BF11TN 16S ribosomal RNA gene, partial sequence
bacteria | 4 leaves
bacteria | 7 leaves
Uncultured bacterium clone BICH787 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone ncd2625b09c1 16S ribosomal RNA gene, partial sequence
Enterobacter sp. UIWRF0151 16S ribosomal RNA gene, partial sequence
Enterobacter sp. NJ-1 16S rRNA gene, strain NJ-1
Pantoea agglomerans strain AJ-G53 16S ribosomal RNA gene, partial sequence
Pantoea septica strain CDDS 8 16S ribosomal RNA gene, partial sequence
Enterobacteriaceae bacterium MR104 16S ribosomal RNA gene, partial sequence
Enterobacter sp. strain B5 gene for 16S rRNA, partial sequence
Enterobacter sp. XJJC-134-3RF2 16S ribosomal RNA gene, partial sequence
Enterobacter sp. IHBB 5017 partial 16S rRNA gene, strain IHBB 5017
Enterobacteriaceae bacterium MR86 16S ribosomal RNA gene, partial sequence
0.002

Stenotrophomomnas rhizophila **KP050794.1**

Stenotrophomonas rhizophila strain HT12-MRL 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KP318062.1| **Length:** 1295 **Number of Matches:** 1

Range 1: 59 to 491 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
760 bits(842)	0.0	429/433(99%)	1/433(0%)	Plus/Plus

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Sbjct  59   GGGTGAGGAATACATCGGAATCTACCTTTTCGTGGGGGATAACGTAGGGAAACTTACGCT  118

Query  96   AATACCGCATACGACCTTCGGGTGAAAGCAGGGGACCTTCGGGCCTTGCGCGGATAGATG  155
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Sbjct  119  AATACCGCATACGACCTTCGGGTGAAAGCAGGGGACCTTCGGGCCTTGCGCGGATAGATG  178

Query  156  AGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCCACCAAGGCGACGATCCGTAGC  215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179  AGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAGGCCCACCAAGGCGACGATCCGTAGC  238

Query  216  TGGTCTGAGAGGATGATCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAG  275
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Query  276  GCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATACCGCGTGGGTG  335
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Query  396  CGGTTGTTCTGACGGTACCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGG  455
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Sbjct  419  CGGTTGTTCTGACGGTACCCAAAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGCGG  478

Query  456  TAATACGAAGGGT  468
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Sbjct  479  TAATACGAAGGGT  491
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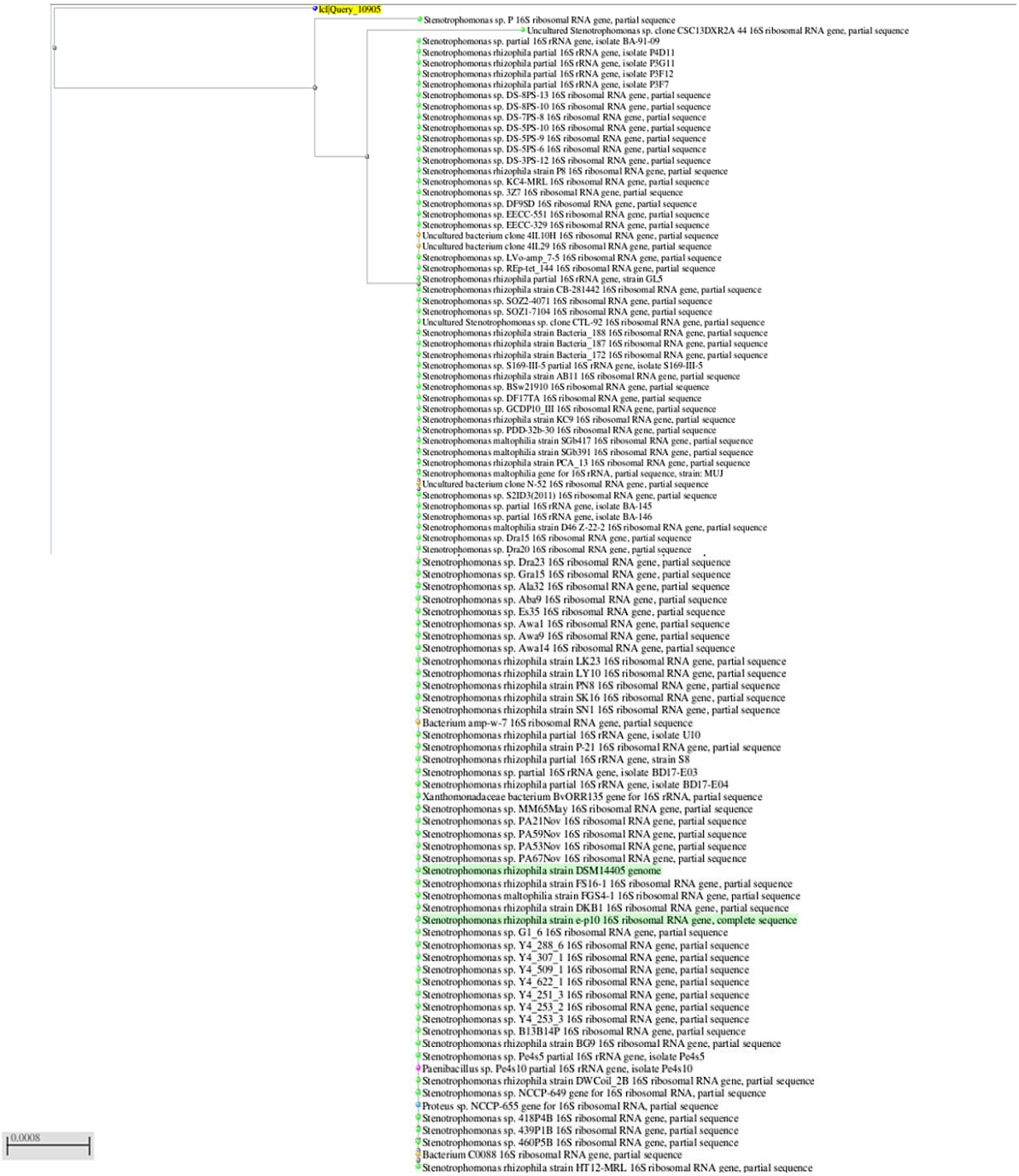
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Stenotrophomonas sp. P 16S ribosomal RNA gene, partial sequence
Uncultured Stenotrophomonas sp. clone CSC13DXR2A 44 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. partial 16S rRNA gene, isolate BA-91-09
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate P4D11
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate P3G11
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate P3F12
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate P3F7
Stenotrophomonas sp. DS-8PS-13 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-8PS-10 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-7PS-8 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-5PS-10 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-5PS-9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-5PS-6 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DS-3PS-12 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain P8 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. KC4-MRL 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 3Z7 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DF9SD 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. EECC-551 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. EECC-329 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 4IL10H 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone 4IL29 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. LVo-amp_7-5 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. REp-tet_144 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila partial 16S rRNA gene, strain GL5
Stenotrophomonas rhizophila strain CB-281442 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. SOZ2-4071 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. SOZ1-7104 16S ribosomal RNA gene, partial sequence
Uncultured Stenotrophomonas sp. clone CTL-92 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain Bacteria_188 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain Bacteria_187 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain Bacteria_172 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. S169-III-5 partial 16S rRNA gene, isolate S169-III-5
Stenotrophomonas rhizophila strain AB11 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. BSw21910 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. DF17TA 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. GCDP10_III 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain KC9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. PDD-32b-30 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain SGb417 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain SGb391 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain PCA_13 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia gene for 16S rRNA, partial sequence, strain: MUJ
Uncultured bacterium clone N-52 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. S2ID3(2011) 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. partial 16S rRNA gene, isolate BA-145
Stenotrophomonas sp. partial 16S rRNA gene, isolate BA-146
Stenotrophomonas maltophilia strain D46 Z-22-2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Dra15 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Dra20 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Dra23 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Gra15 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Ala32 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Aba9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Es35 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Awa1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Awa9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Awa14 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain LK23 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain LY10 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain PN8 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain SK16 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain SN1 16S ribosomal RNA gene, partial sequence
Bacterium amp-w-7 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate U10
Stenotrophomonas rhizophila strain P-21 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila partial 16S rRNA gene, strain S8
Stenotrophomonas sp. partial 16S rRNA gene, isolate BD17-E03
Stenotrophomonas rhizophila partial 16S rRNA gene, isolate BD17-E04
Xanthomonadaceae bacterium BvORR135 gene for 16S rRNA, partial sequence
Stenotrophomonas sp. MM65May 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. PA21Nov 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. PA59Nov 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. PA53Nov 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. PA67Nov 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain DSM14405 genome
Stenotrophomonas rhizophila strain FS16-1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas maltophilia strain FGS4-1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain DKB1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain e-p10 16S ribosomal RNA gene, complete sequence
Stenotrophomonas sp. G1_6 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_288_6 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_307_1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_509_1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_622_1 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_251_3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_253_2 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Y4_253_3 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. B13B14P 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain BG9 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. Pe4s5 partial 16S rRNA gene, isolate Pe4s5
Paenibacillus sp. Pe4s10 partial 16S rRNA gene, isolate Pe4s10
Stenotrophomonas rhizophila strain DWCoil_2B 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. NCCP-649 gene for 16S ribosomal RNA, partial sequence
Proteus sp. NCCP-655 gene for 16S ribosomal RNA, partial sequence
Stenotrophomonas sp. 418P4B 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 439P1B 16S ribosomal RNA gene, partial sequence
Stenotrophomonas sp. 460P5B 16S ribosomal RNA gene, partial sequence
Bacterium C0088 16S ribosomal RNA gene, partial sequence
Stenotrophomonas rhizophila strain HT12-MRL 16S ribosomal RNA gene, partial sequence
0.0008

Citrobacter freundii CP007557

Citrobacter freundii CFNIH1, complete genome

Sequence ID: gb|CP007557.1| **Length:** 5099034 **Number of Matches:** 1

Range 1: 5039222 to 5039628 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
477 bits(528)	6e-131	353/408(87%)	3/408(0%)	Plus/Plus

Features: hypothetical protein
phospho-2-dehydro-3-deoxyheptonate aldolase

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Query  121      CAGTGTTATTTTAAGGCAAAAATAGCCCTT-ATAAATGTACACTTAAATTTACACCA-CG  178
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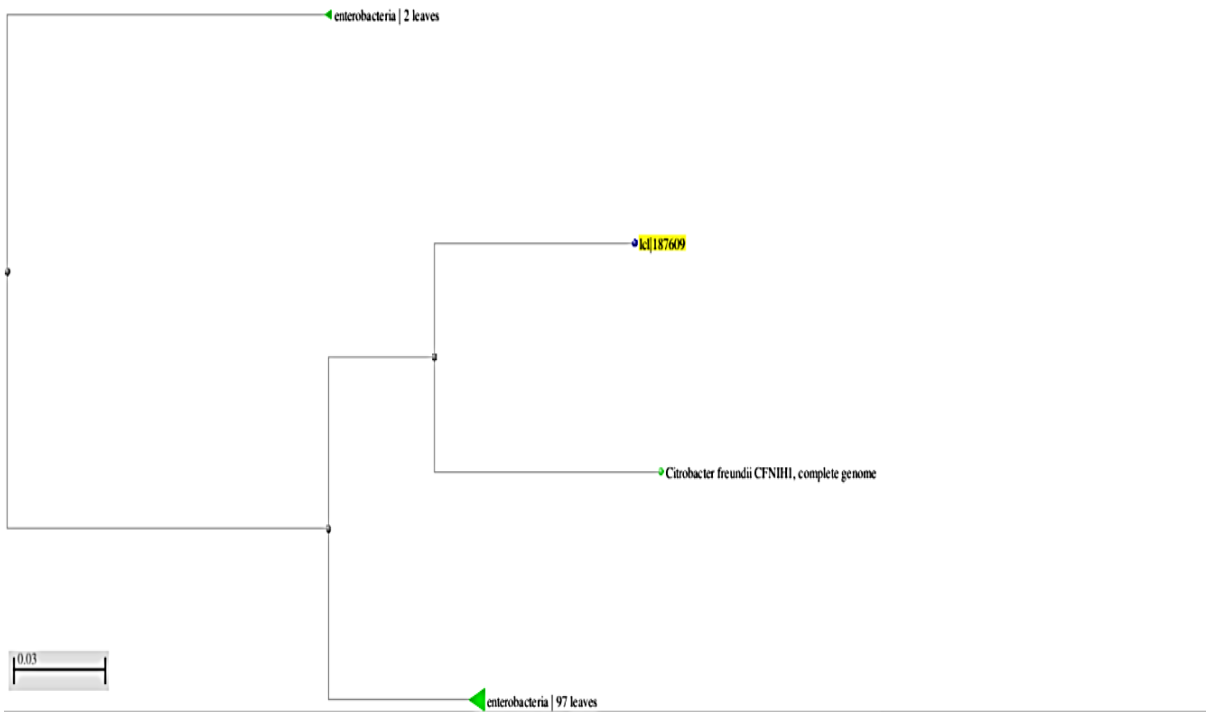
enterobacteria | 2 leaves
kl|187609
Citrobacter freundii CFNIH1, complete genome
0.03
enterobacteria | 97 leaves

Pseudomonas frederiksbergensis EU373369.1

Pseudomonas frederiksbergensis strain PR18 16S ribosomal RNA gene, partial sequence

Sequence ID: gb|KJ870030.1| Length: 1449 Number of Matches: 1

Range 1: 832 to 1350 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
919 bits(1018)	0.0	515/519(99%)	0/519(0%)	Plus/Minus

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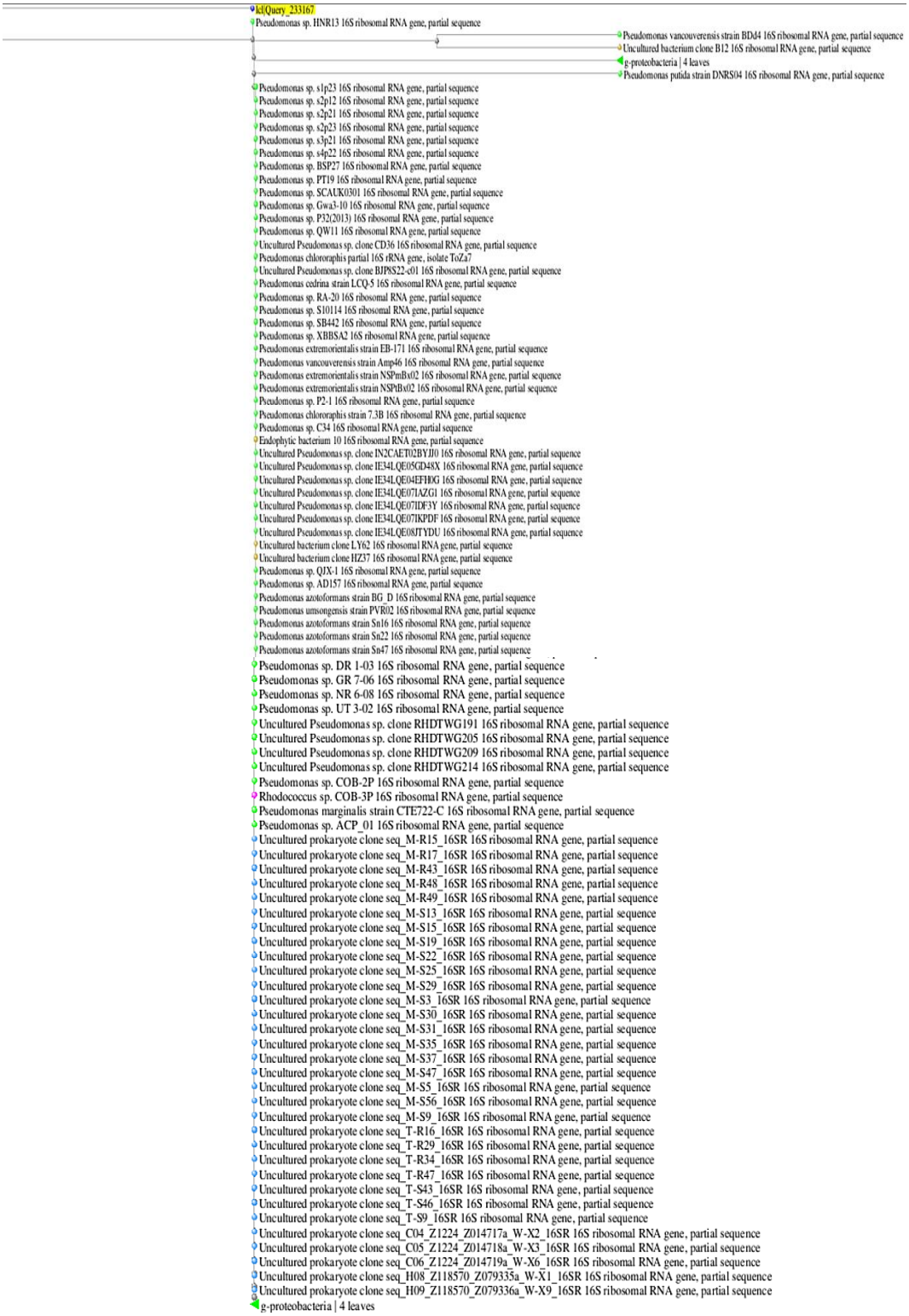
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Pseudomonas sp. HNR13 16S ribosomal RNA gene, partial sequence
Pseudomonas vancouverensis strain BDd4 16S ribosomal RNA gene, partial sequence
Uncultured bacterium clone B12 16S ribosomal RNA gene, partial sequence
g-proteobacteria | 4 leaves
Pseudomonas putida strain DNRS04 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s1p23 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s2p12 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s2p21 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s2p23 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s3p21 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. s4p22 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. BSP27 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. PT19 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. SCAUK0301 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. Gwa3-10 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. P32(2013) 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. QW11 16S ribosomal RNA gene, partial sequence
Uncultured Pseudomonas sp. clone CD36 16S ribosomal RNA gene, partial sequence
Pseudomonas chlororaphis partial 16S rRNA gene, isolate ToZa7
Uncultured Pseudomonas sp. clone BJP8S22-c01 16S ribosomal RNA gene, partial sequence
Pseudomonas cedrina strain LCQ-5 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. RA-20 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. S10114 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. SB442 16S ribosomal RNA gene, partial sequence
Pseudomonas sp. XBBSA2 16S ribosomal RNA gene, partial sequence
Pseudomonas extremorientalis strain EB-171 16S ribosomal RNA gene, partial sequence
Pseudomonas vancouverensis strain Amp46 16S ribosomal RNA gene, partial sequence
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Pseudomonas sp. P2-1 16S ribosomal RNA gene, partial sequence
Pseudomonas chlororaphis strain 7.3B 16S ribosomal RNA gene, partial sequence
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Pseudomonas azotoformans strain Sn22 16S ribosomal RNA gene, partial sequence
Pseudomonas azotoformans strain Sn47 16S ribosomal RNA gene, partial sequence
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Pseudomonas sp. GR 7-06 16S ribosomal RNA gene, partial sequence
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Pseudomonas sp. UT 3-02 16S ribosomal RNA gene, partial sequence
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Rhodococcus sp. COB-3P 16S ribosomal RNA gene, partial sequence
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g-proteobacteria | 4 leaves